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=> d que
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L2             2 SEA FILE=REGISTRY ABB=ON  PLU=ON  ("PR 39"/CN OR "PR 39 (ION
                 EXCHANGER)"/CN OR "PR 39 (PEPTIDE)"/CN)
L4            53 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1 AND (L2 OR PR39 OR PR 39)
L5          8645 SEA FILE=HCAPLUS ABB=ON  PLU=ON  ANGIOGENESIS+NT/CT
L6             6 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1 AND (L5 OR ANGIOGEN?)
L7             6 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L4 AND (L5 OR ANGIOGEN?)
L8             6 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L6 OR L7


=> d ibib abs hitstr 18 1-6

L8   ANSWER 1 OF 6  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2002:220416  HCAPLUS
DOCUMENT NUMBER:          136:257252
TITLE:                    Method of modulating neovascularization
INVENTOR(S):              Kovesdi, Imre
PATENT ASSIGNEE(S):       Genvec, Inc., USA
SOURCE:                   PCT Int. Appl., 33 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
     WO 2002022176      A1   20020321      WO 2001-US28954  20010914
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT,
             RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ,
             VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
             BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
     AU 2001091019      A5   20020326      AU 2001-91019    20010914
PRIORITY APPLN. INFO.:                   US 2000-233001P  P  20000915
                                         WO 2001-US28954  W  20010914
AB   The present invention provides a method of modulating neovascularization
     in an animal.  The method comprises administering tot he animal two or
     more nucleic acid sequences, each nucleic acid sequence encoding at least
     one angiogenesis-modulation factor that acts upon a different
     angiogenic process, such that the nucleic acid sequences are
     expressed to produce the angiogenesis-modulation factors to
     modulate neovascularization in the animal.  Modulating neovascularization
     includes the induction of neovascularization or, in the alternative, the
     inhibition or redn. of neovascularization.
IT   139637-11-9, PR39 peptide
     RL: BUU (Biological use, unclassified); PAC (Pharmacological activity);
     BIOL (Biological study); USES (Uses)
        (method of modulating neovascularization)
RN   139637-11-9  HCAPLUS
CN   L-Prolinamide, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-
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prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-prolyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-leucyl-L-prolyl-L-prolyl-L-arginyl-L-isoleucyl-L-prolyl-L-prolylglycyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:319740 HCAPLUS
DOCUMENT NUMBER: 134:336214
TITLE: Method for **PR-39** peptide regulated stimulation of **angiogenesis**
INVENTOR(S): Simons, Michael; Gao, Youhe
PATENT ASSIGNEE(S): Beth Israel Deaconess Medical Center, USA
SOURCE: PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001030368	A1	20010503	WO 2000-US27552	20001006

W: AU, CA, JP
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.: US 1999-426011 A 19991025

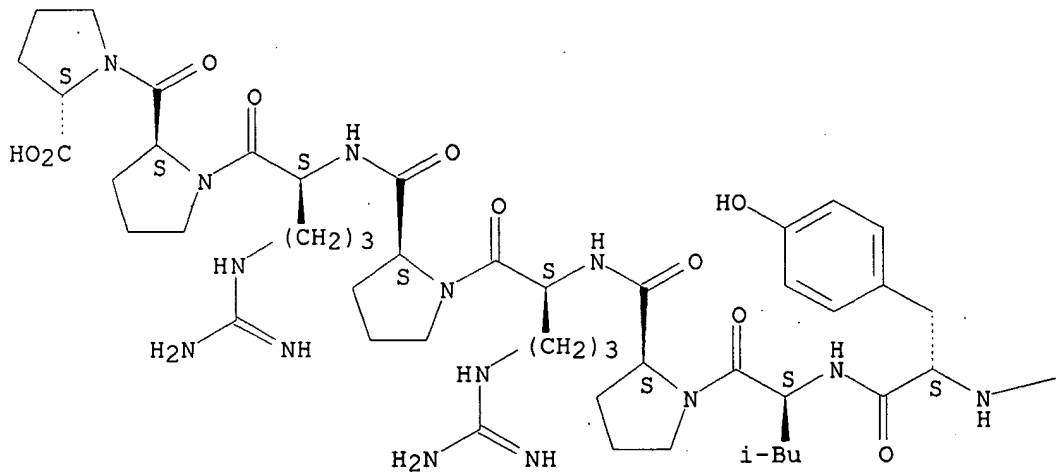
AB The present invention provides both a method and means for regulating **angiogenesis** within living cells, tissues, and organs in-situ. The regulation is performed using native **PR-39** peptide or one of its shorter-length homolog, for interaction with such proteasomes as one present in the cytoplasm of viable cells. The result of **PR-39** peptide interaction with proteasomes is a decrease in the intracellular degrdn. of active peptides such as HIF-1.alpha. and a consequential stimulation of **angiogenesis** in-situ.

IT **298702-64-4**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(**PR-39** peptide regulated stimulation of **angiogenesis**)

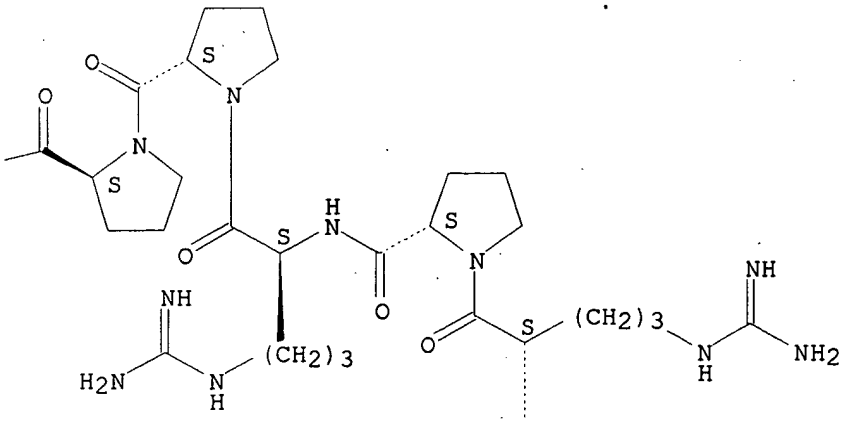
RN 298702-64-4 HCAPLUS
CN L-Proline, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



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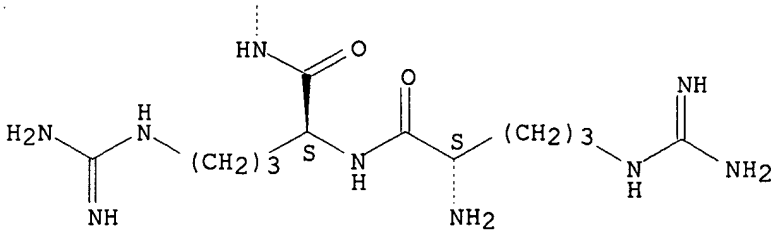


IT **139637-11-9, PR-39** peptide
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**PR-39** peptide regulated stimulation of **angiogenesis**)
RN 139637-11-9 HCAPLUS
CN L-Prolinamide, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-prolyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-leucyl-L-prolyl-L-prolyl-L-arginyl-L-isoleucyl-L-prolyl-L-prolylglycyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:706997 HCAPLUS
DOCUMENT NUMBER: 133:276343
TITLE: Method for **PR-39** peptide regulated stimulation of **angiogenesis**
INVENTOR(S): Simons, Michael; Gao, Youhe
PATENT ASSIGNEE(S): Beth Israel Deaconess Medical Center, USA
SOURCE: PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000057895	A1	20001005	WO 2000-US7050	20000316
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1165111	A1	20020102	EP 2000-919442	20000316
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1999-276868 A 19990326
WO 2000-US7050 W 20000316

AB The present invention provides both a method and means for regulating **angiogenesis** within living cells, tissues, and organs in-situ. The regulation is performed using native **PR-39** peptide

or one of its shorter-length homologs, for interaction with such proteasomes as one present in the cytoplasm of viable cells. The result of **PR-39** peptide interaction with proteasomes is a decrease in the intracellular degrdn. of active peptides such as HIF-1.alpha. and a consequential stimulation of **angiogenesis** in-situ.

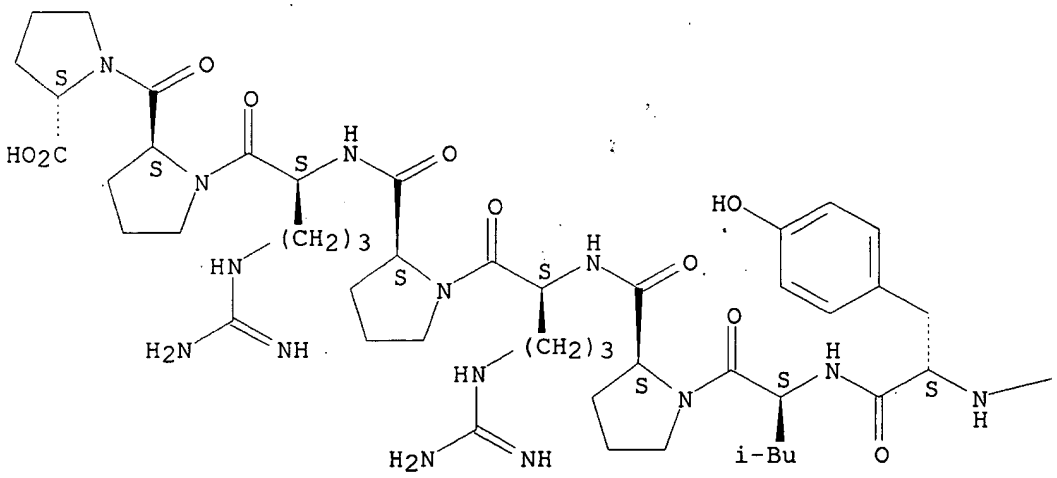
IT **298702-64-4P**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PNU (Preparation, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(**PR-39** peptide-regulated stimulation of **angiogenesis**)

RN 298702-64-4 HCAPLUS

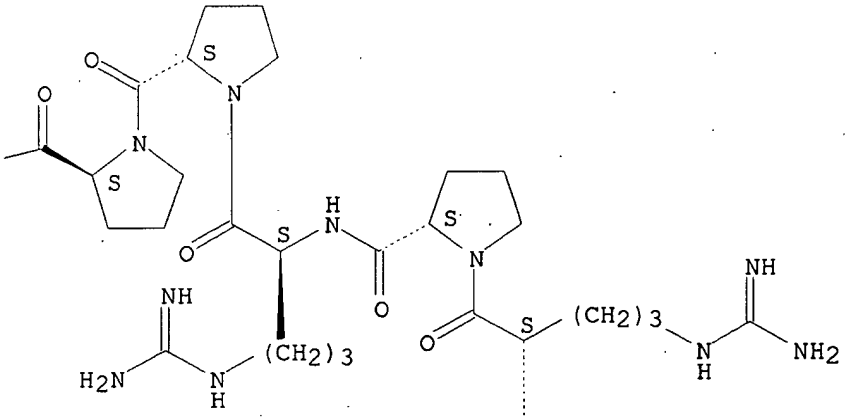
CN L-Proline, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

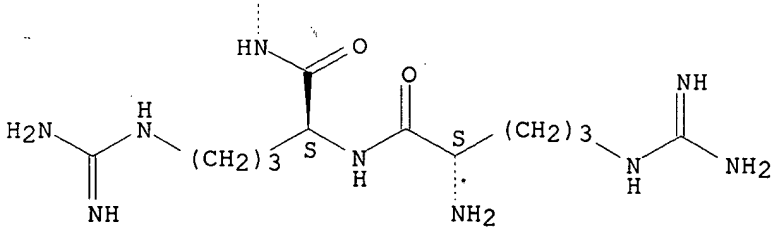
PAGE 1-A



PAGE 1-B



PAGE 2-B



IT **148046-54-2**
RL: PRP (Properties)
(unclaimed protein sequence; method for **PR-39** peptide regulated stimulation of **angiogenesis**)
RN 148046-54-2 HCAPLUS
CN L-Proline, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-prolyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-leucyl-L-prolyl-L-prolyl-L-arginyl-L-isoleucyl-L-prolyl-L-prolylglycyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:178321 HCAPLUS

DOCUMENT NUMBER: 133:205925
TITLE: **PR39**, a peptide regulator of **angiogenesis**. [Erratum to document cited in CA132:149677]
AUTHOR(S): Li, Jian; Post, Mark; Volk, Rudiger; Gao, Youhe; Li, Min; Metals, Caroline; Sato, Kaori; Tsai, Jo; Aird, William; Rosenberg, Robert D.; Hampton, Thomas G.; Li, Jianyi; Sellke, Frank; Carmeliet, Peter; Simons, Michael
CORPORATE SOURCE: Angiogenesis Research Center, Department of Surgery, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA, 02215, USA
SOURCE: Nature Medicine (New York) (2000), 6(3), 356
CODEN: NAMEFI; ISSN: 1078-8956
PUBLISHER: Nature America
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The correct versions are given for Figs. 2a, c, and d on page 51; Fig. 3c on page 52; and Fig. 5b on page 53.
IT **139637-11-9, PR-39**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**PR39** peptide in regulation of **angiogenesis** by inhibiting ubiquitin-proteasome-dependent degrdn. of hypoxia-inducible factor-1.alpha. protein (Erratum))
RN 139637-11-9 HCAPLUS
CN L-Prolinamide, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-prolyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-leucyl-L-prolyl-L-prolyl-L-arginyl-L-isoleucyl-L-prolyl-L-prolylglycyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L8 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:46162 HCAPLUS
DOCUMENT NUMBER: 132:149677
TITLE: **PR39**, a peptide regulator of **angiogenesis**
AUTHOR(S): Li, Jian; Post, Mark; Volk, Rudiger; Gao, Youhe; Li, Min; Metais, Caroline; Sato, Kaori; Tsai, Jo; Aird, William; Rosenberg, Robert D.; Hampton, Thomas G.; Li, Jianyi; Sellke, Frank; Carmeliet, Peter; Simons, Michael
CORPORATE SOURCE: Angiogenesis Research Center, Department of Surgery both at Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA, 02215, USA
SOURCE: Nature Medicine (New York) (2000), 6(1), 49-55
CODEN: NAMEFI; ISSN: 1078-8956
PUBLISHER: Nature America
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Although tissue injury and inflammation are considered essential for the induction of **angiogenesis**, the mol. controls of this cascade are mostly unknown. Here we show that a macrophage-derived peptide,

PR39, inhibited the ubiquitin-proteasome-dependent degrdn. of hypoxia-inducible factor-1.alpha. protein, resulting in accelerated formation of vascular structures in vitro and increased myocardial vasculature in mice. For the latter, coronary flow studies demonstrated that **PR39**-induced **angiogenesis** resulted in the prodn. of functional blood vessels. These findings show that **PR39** and related compds. can be used as potent inductors of **angiogenesis**, and that selective inhibition of hypoxia-inducible factor-1.alpha. degrdn. may underlie the mechanism of inflammation-induced **angiogenesis**.

IT **139637-11-9, PR-39**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**PR39** peptide in regulation of **angiogenesis** by inhibiting ubiquitin-proteasome-dependent degrdn. of hypoxia-inducible factor-1.alpha. protein)

RN 139637-11-9 HCAPLUS

CN L-Prolinamide, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-prolyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-leucyl-L-prolyl-L-prolyl-L-arginyl-L-isoleucyl-L-prolyl-L-prolylglycyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 6 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1996:357168 HCAPLUS
DOCUMENT NUMBER: 125:26311
TITLE: Synducin (syndecan expression-inducers) mediate modulation of tissue repair
INVENTOR(S): Gallo, Richard L.; Bernfield, Merton
PATENT ASSIGNEE(S): Children's Medical Center Corporation, USA
SOURCE: PCT Int. Appl., 32 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9609322	A2	19960328	WO 1995-US12080	19950922
WO 9609322	A3	19960523		
W: AU, CA, JP, KR				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5654273	A	19970805	US 1994-310722	19940922
AU 9538228	A1	19960409	AU 1995-38228	19950922
US 5863897	A	19990126	US 1996-728333	19961010

PRIORITY APPLN. INFO.: US 1994-310722 19940922
WO 1995-US12080 19950922

AB The membrane-permeating antibacterial peptide, **PR-39**, previously found only in the intestine, was purified from wound fluid and shown to possess syndecan-1 and syndecan-4 inductive activity specifically in mesenchymal cells. This is a newly recognized function that defines

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peptide contg. syndecan-inducing activity, and that are known as synducins. Therefore, a mol. with both antimicrobial and synducin activities is deposited in wounds where it can simultaneously reduce infection and the influence the action of growth factors, matrix components, and other cellular effectors involved in wound repair. Synducins, including **PR-39**, and derivs. thereof, as well as other proline and arginine-rich antimicrobial peptides, collectively referred to herein as "synducins", are therefore useful in the modulation of wound healing, as well as other disorders involving mesenchymal cells and cell surface mol. interaction, including metastatic disease, **angiogenesis**, restenosis, stasis or decubitis ulcers, and prevention of keloids.

IT **139637-11-9**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(synducins are syndecan expression-inducing peptides that mediate modulation of mesenchymal tissue repair)

RN 139637-11-9 HCAPLUS

CN L-Prolinamide, L-arginyl-L-arginyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-tyrosyl-L-leucyl-L-prolyl-L-arginyl-L-prolyl-L-arginyl-L-prolyl-L-prolyl-L-prolyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-leucyl-L-prolyl-L-prolyl-L-arginyl-L-isoleucyl-L-prolyl-L-prolylglycyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl-L-prolyl-L-prolyl-L-arginyl-L-phenylalanyl- (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	90	100.0	15	22	AAB84691	Amino acid sequenc
3	90	100.0	15	22	AAB97277	PR-39 derived pept
4	90	100.0	19	17	AAW01452	Leukocyte O2- prod
5	90	100.0	26	17	AAW01447	Leukocyte O2- prod
6	90	100.0	26	19	AAW75723	Proline/Arginine r
7	90	100.0	39	14	AAR30491	Antibacterial pept
8	90	100.0	39	17	AAW01446	Leukocyte O2- prod
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10	90	100.0	39	17	AAR99121	Magainin-derived a
11	90	100.0	39	19	AAW75722	Proline/Arginine r
12	90	100.0	39	21	AAB26888	PR-39 peptide used
13	90	100.0	39	22	AAB84690	Amino acid sequenc
14	90	100.0	39	22	AAB97280	PR-39 peptide. Un
15	90	100.0	42	23	ABB07714	Antimicrobial pept
16	90	100.0	44	22	AAB51194	E. coli AMP gene P
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18	83	92.2	14	19	AAW75725	Proline/Arginine r
19	75	83.3	23	17	AAW01451	Leukocyte O2- prod
20	66	73.3	18	16	AAR79211	Bactenecin peptide
21	66	73.3	20	19	AAW75730	Proline/Arginine r
22	66	73.3	23	16	AAR79209	Bactenecin peptide
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24	66	73.3	59	19	AAW66400	Cationic peptide B
25	66	73.3	59	21	AAY91699	Cationic peptide B
26	66	73.3	60	23	ABB07713	Antimicrobial pept
27	66	73.3	62	22	AAB51197	E. coli AMP gene B
28	64	71.1	11	21	AAB26886	PR-39 derived angi
29	64	71.1	11	22	AAB84692	Amino acid sequenc
30	64	71.1	11	22	AAB97278	PR-39 derived pept
31	63	70.0	91	22	AAU61229	Propionibacterium
32	61	67.8	336	17	AAW05520	HCMV Toledo strain
33	60	66.7	953	23	AAU74761	Human protease PRT
34	60	66.7	953	23	AAU82708	Amino acid sequenc
35	59	65.6	39	21	AAB44779	Human secreted pro
36	59	65.6	59	17	AAR94448	Synducin peptide (
37	56.5	62.8	74	22	ABB42619	Peptide #10125 enc
38	56.5	62.8	74	22	AAM63510	Human brain expres
39	56.5	62.8	74	22	AAM76324	Human bone marrow
40	56.5	62.8	74	22	AAM36433	Peptide #10470 enc
41	56.5	62.8	74	23	ABG45621	Human peptide enco
42	56	62.2	692	22	AAU04851	Micromonospora eve
43	55.5	61.7	497	20	AAY04972	Mycobacterium spec
44	55	61.1	45	22	AAM18621	Peptide #5055 enco
45	54	60.0	87	22	AAU53075	Propionibacterium

ALIGNMENTS

RESULT 1
AAB26885
ID AAB26885 standard; peptide; 15 AA.
XX
AC AAB26885;
XX
DT 01-FEB-2001 (first entry)
XX
DE PR-39 derived angiogenesis regulatory peptide 1.
XX
KW Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
KW myocardial ischaemia; proteasome.
XX
OS Synthetic.
XX
PN WO200057895-A1.
XX
PD 05-OCT-2000.
XX
PF 16-MAR-2000; 2000WO-US07050.
XX
PR 26-MAR-1999; 99US-0276868.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2000-628319/60.
XX
PT Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
PT infarction, by administering a PR-39 oligopeptide that regulates
PT enzymatic activity of proteosomes -
XX

PS Claim 12; Page 40; 51pp; English.
XX
CC This invention relates to a method for the stimulation of angiogenesis in
CC situ within a targeted collection of viable cells. The method comprises
CC introducing, into the cytoplasm, at least 1 member of the PR-39
CC oligopeptide collective, which interacts with cytoplasmic proteasomes.
CC Part of the proteolytic activity of the proteosomes is selectively
CC altered so as to stimulate angiogenesis. The method is used to induce
CC angiogenesis in tissue that has suffered anoxia or infarction,
CC e.g. myocardial infarction or chronic myocardial ischaemia, and also to
CC study the mechanisms that control angiogenesis. The present sequence
CC represents a PR-39 derived peptide which interacts with the proteasome
CC and can be used in the method of the invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 90; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 2
AAB84691
ID AAB84691 standard; peptide; 15 AA.
XX
AC AAB84691;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a PR-39 derived peptide (residues 1-15).
XX
KW PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
KW myocardial infarction; chronic myocardial ischemia; heart disease;
KW anoxia.
XX
OS Unidentified.
XX
PN WO200147540-A1.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-US35293.
XX
PR 29-DEC-1999; 99US-0474967.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2001-441690/47.
XX
PT Selective inhibition of IkappaBalpha degradation within targeted viable
PT cell collection, involves interacting PR-39 oligopeptide with
PT IkappaBalpha and proteasomes, and altering proteolytic activity of
PT proteasomes -
XX
PS Claim 11; Page 58; 69pp; English.
XX
CC The present sequence represents a PR-39 derived peptide. It is used
CC for selective inhibition of IkappaBalpha degradation within a targeted
CC cell collection in-situ. The method is useful for selectively inhibiting
CC IkappaBalpha protein degradation in situ, decreasing the activity of
CC NFkappaB transcription factor and selective control of NFkappaB-dependent
CC gene expression in situ. The PR-39 derived peptides are useful in the
CC treatment of myocardial infarction, chronic myocardial ischemia of
CC heart disease and anoxia.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 90; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 3
AAB97277
ID AAB97277 standard; peptide; 15 AA.
XX
AC AAB97277;
XX
DT 09-AUG-2001 (first entry)
XX
DE PR-39 derived peptide PR-15.
XX
KW PR-39; cathelin; inflammation; wound healing; myocardial infarction;
KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;
KW anoxia; chronic myocardial ischaemia; heart tissue.
XX
OS Unidentified.
XX
PN WO200130368-A1.
XX
PD 03-MAY-2001.
XX
PF 06-OCT-2000; 2000WO-US27552.
XX
PR 25-OCT-1999; 99US-0426011.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2001-355179/37.
XX
PT Stimulation of angiogenesis and inhibition of proteasome mediated
PT degradation in cells, by introduction of PR-39 oligopeptide or its
PT N-terminal fragments or their conjugates, for use in anoxia and
PT infarction conditions -
XX
PS Claim 12; Page 42; 52pp; English.
XX
CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39
CC is a member of the the cathelin family of proteins, mature PR-39 is 39
CC amino acids in length (see AAB97280), and has been shown to play a role
CC in several inflammatory events including wound healing and myocardial
CC infarction. The PR-39 derived family of oligopeptides cause selective
CC inhibition of proteasome mediated degeneration of peptides and
CC stimulation of angiogenesis after their intracellular introduction to a
CC target cell. PR-39 derived peptides are able to interact with at least
CC the alpha7 subunit of the proteasomes, and therefore alter the
CC proteolytic activity of proteasomes such that a selective increased
CC expression of specific proteins occurs. The invention includes methods
CC for the selective inhibition of proteasome mediated peptide degradation.
CC The method provides means for stimulating angiogenesis as required in
CC living tissues and organs which have suffered defects or have undergone
CC anoxia and/or infarction, myocardial infarction or chronic myocardial
CC ischaemia of heart tissue. Examples are the myocardium, skeletal or
CC smooth muscle, artery or vein, lung, brain, kidney, spleen, liver,
CC gastrointestinal or nerve tissues, limbs, and extremities. A particular
CC example is after myocardial infarction or ischaemia.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 90; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15

```
          ||||||||||||||||
Db        1 RRRPRPPYLPRPRPP 15


RESULT 4
AAW01452
ID   AAW01452 standard; peptide; 19 AA.
XX
AC   AAW01452;
XX
DT   18-JUN-1997  (first entry)
XX
DE   Leukocyte O2- production inhibitor peptide PR19.
XX
KW   Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
KW   antimicrobial peptide; small intestine; human; neutrophil; bacteria;
KW   DNA synthesis; protein synthesis; inhibitor; syndecan expression;
KW   mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
KW   tissue damage; oxygen radical; inflammatory disease; therapy.
XX
OS   Synthetic.
XX
PN   WO9632129-A1.
XX
PD   17-OCT-1996.
XX
PF   10-APR-1996;   96WO-US04674.
XX
PR   10-APR-1995;   95US-0419066.
XX
PA   (UNIV ) UNIV KANSAS STATE RES FOUND.
XX
PI   Blecha F,  Shi J;
XX
DR   WPI; 1996-476842/47.
XX
PT   Inhibition of leukocyte super:oxide anion prodn. and attraction of
PT   leukocytes - using peptide(s) partic. based on antimicrobial PR-39
XX
PS   Disclosure; Page 27; 45pp; English.
XX
CC   AAW01447-W01454 represent fragments of the proline-arginine rich
CC   antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
CC   isolated from porcine small intestine, and has also been identified in
CC   human and porcine neutrophils. PR39 kills bacteria by interfering with
CC   DNA and/or protein synthesis. PR39 also induces syndecan expression on
CC   mesenchymal cells. Syndecans are important in wound repair, showing that
CC   PR39 can be used in wound repair, as well as in antibacterial agents.
CC   These sequences, and PR39, can be used in the method of the invention.
CC   The method of the invention is for inhibiting leukocyte superoxide anion
CC   (O2-) production. The method comprises administering to a leukocyte a
CC   peptide (such as this sequence) capable of inhibiting leukocyte O2-
CC   production. The peptides can be used as medicaments for fighting
CC   infection by attracting leukocytes to a wound site and restricting
CC   tissue damage at the wound site caused by excessive oxygen radicals
CC   produced by these leukocytes. They can also be used to develop products
CC   for treating inflammatory disease states.
XX
SQ   Sequence   19 AA;

  Query Match             100.0%;  Score 90;  DB 17;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 RRRPRPPYLPRPRPP 15
          ||||||||||||||||
Db        1 RRRPRPPYLPRPRPP 15


RESULT 5
AAW01447
ID   AAW01447 standard; peptide; 26 AA.
XX
AC   AAW01447;
XX
DT   18-JUN-1997  (first entry)
XX
DE   Leukocyte O2- production inhibitor peptide PR26.
XX
KW   Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
KW   antimicrobial peptide; small intestine; human; neutrophil; bacteria;
KW   DNA synthesis; protein synthesis; inhibitor; syndecan expression;
KW   mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
KW   tissue damage; oxygen radical; inflammatory disease; therapy.
XX
OS   Synthetic.
XX
PN   WO9632129-A1.
XX
PD   17-OCT-1996.
XX
PF   10-APR-1996;   96WO-US04674.
XX
PR   10-APR-1995;   95US-0419066.
XX
PA   (UNIV ) UNIV KANSAS STATE RES FOUND.
XX
PI   Blecha F,  Shi J;
XX
DR   WPI; 1996-476842/47.
XX
PT   Inhibition of leukocyte super:oxide anion prodn. and attraction of
PT   leukocytes - using peptide(s) partic. based on antimicrobial PR-39
XX
PS   Claim 3; Page 26; 45pp; English.
XX
CC   AAW01447-W01454 represent fragments of the proline-arginine rich
CC   antimicrobial peptide PR39 (see AAW01446). The PR39 sequence was first
CC   isolated from porcine small intestine, and has also been identified in
CC   human and porcine neutrophils. PR39 kills bacteria by interfering with
CC   DNA and/or protein synthesis. PR39 also induces syndecan expression on
CC   mesenchymal cells. Syndecans are important in wound repair, showing that
CC   PR39 can be used in wound repair, as well as in antibacterial agents.
CC   These sequences, and PR39, can be used in the method of the invention.
CC   The method of the invention is for inhibiting leukocyte superoxide anion
CC   (O2-) production. The method comprises administering to a leukocyte a
CC   peptide (such as this sequence) capable of inhibiting leukocyte O2-
CC   production. The peptides can be used as medicaments for fighting
CC   infection by attracting leukocytes to a wound site and restricting
CC   tissue damage at the wound site caused by excessive oxygen radicals
CC   produced by these leukocytes. They can also be used to develop products
CC   for treating inflammatory disease states.
XX
SQ   Sequence   26 AA;

  Query Match             100.0%;  Score 90;  DB 17;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.00033;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 RRRPRPPYLPRPRPP 15
          ||||||||||||||||
Db        1 RRRPRPPYLPRPRPP 15


RESULT 6
AAW75723
ID   AAW75723 standard; peptide; 26 AA.
XX
AC   AAW75723;
XX
DT   19-NOV-1998  (first entry)
XX
DE   Proline/Arginine rich peptide PR-26.
XX
KW   Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
KW   superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
```

KW coronary bypass; organ transplantation surgery.
XX
OS Synthetic.
XX
PN WO9835690-A1.
XX
PD 20-AUG-1998.
XX
PF 17-FEB-1998; 98WO-US03207.
XX
PR 16-FEB-1998; 98US-0024975.
PR 18-FEB-1997; 97US-0802306.
XX
PA (UNIV) UNIV KANSAS STATE RES FOUND.
XX
PI Blecha F, Ross CR, Shi J;
XX
DR WPI; 1998-495359/42.
XX
PT Reduction of reperfusion injury in temporarily occluded blood
PT vessels - by administration of a peptide which is rich in proline
PT or arginine residues
XX
PS Claim 3; Page 14-15; 35pp; English.
XX
CC Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
CC administration into a mammal's bloodstream reduce reperfusion injury
CC (production of reactive oxygen species, neutrophil adherence to
CC endothelium, and extravasation of neutrophils). These peptides have two
CC requirements: they contain the consensus sequence PXXP, where P is a
CC proline residue and X is any amino acid residue, which has been found to
CC inhibit superoxide production, and secondly they have arginine residues
CC adjacent to these motifs, required for effective inhibition. It was
CC established by structural and function analysis that a peptide should
CC ideally contain 4 or 6 of these motifs, and that inhibitory activity is
CC correlated with the increase of length of peptides. The effectiveness
CC of these peptides was determined by investigating the production of the
CC neutrophil superoxide anion, and also the inhibition of neutrophil
CC chemotaxis. From this, it was found that all of the peptides inhibited
CC NADPH oxidase to some extent. All of the peptides also inhibit
CC neutrophil oxidase activity. PR-39 is believed, to be the most potent
CC endogenous down regulator of NADPH oxidase yet discovered, and from the
CC data produced, it can be suggested to be involved in eliminating or
CC reducing the reperfusion injury induced adhesion and extraction of
CC neutrophils. The peptides are also useful in connection with surgical
CC procedures such as coronary bypass and organ transplantation surgery.
XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 90; DB 19; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 7
AAR30491
ID AAR30491 standard; peptide; 39 AA.
XX
AC AAR30491;
XX
DT 12-MAY-1993 (first entry)
XX
DE Antibacterial peptide.
XX
KW Pig; small intestine; endocrine; gram negative; bacteria; therapeutic;
KW veterinary medicine; prophylactic.
XX
OS Sus scrofa domestica.
XX
PN WO9222578-A.
XX
PD 23-DEC-1992.
XX
PF 10-JUN-1992; 92WO-SE00394.
XX
PR 14-JUN-1991; 91SE-0001838.
XX
PA (BOMA/) BOMAN H G.
PA (JOER/) JOERNVALL H.
PA (LEEJ/) LEE J.
PA (MUTT/) MUTT V.
XX
PI Boman HG, Joernvall H, Lee J, Mutt V;
XX
DR WPI; 1993-018080/02.
XX
PT New anti-bacterial polypeptide - active against Gram negative
PT bacteria
XX
PS Claim 1; Page 10; 15pp; English.
XX
CC This peptide was isolated from the small intestine of a pig. The
CC small inestine is an important endocrine organ and many
CC physiologically active peptides have been isolated from it. This
CC peptide inhibits the growth of, and may kill, bacteria, pref. gram
CC negative bacteria. This peptide or its functional derivatives may be
CC used in human or veterinary medicine for therapeutic or prophylactic
CC use.
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 90; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 8
AAW01446
ID AAW01446 standard; peptide; 39 AA.
XX
AC AAW01446;
XX
DT 18-JUN-1997 (first entry)
XX
DE Leukocyte O2- production inhibitor peptide PR39.
XX
KW Inhibitor; leukocyte O2- production; proline-arginine rich peptide; pig;
KW antimicrobial peptide; small intestine; human; neutrophil; bacteria;
KW DNA synthesis; protein synthesis; inhibitor; syndecan expression;
KW mesenchymal cell; wound repair; superoxide anion; infection; leukocyte;
KW tissue damage; oxygen radical; inflammatory disease; therapy.
XX
OS Synthetic.
XX
PN WO9632129-A1.
XX
PD 17-OCT-1996.
XX
PF 10-APR-1996; 96WO-US04674.
XX
PR 10-APR-1995; 95US-0419066.
XX
PA (UNIV) UNIV KANSAS STATE RES FOUND.
XX
PI Blecha F, Shi J;
XX
DR WPI; 1996-476842/47.
XX

PT Inhibition of leukocyte super:oxide anion prodn. and attraction of
PT leukocytes - using peptide(s) partic. based on antimicrobial PR-39
XX
PS Claim 2; Page 26; 45pp; English.
XX
CC This sequence represents the proline-arginine rich antimicrobial peptide
CC PR39. The PR39 sequence was first isolated from porcine small intestine,
CC and has also been identified in human and porcine neutrophils. PR39
CC kills bacteria by interfering with DNA and/or protein synthesis. PR39
CC also induces syndecan expression on mesenchymal cells. Syndecans are
CC important in wound repair, showing that PR39 can be used in wound repair,
CC as well as in antibacterial agents. This sequence, and the fragments of
CC it shown in AAW01447-W01454, can be used in the method of the invention.
CC The method of the invention is for inhibiting leukocyte superoxide anion
CC (O2-) production. The method comprises administering to a leukocyte a
CC peptide (such as this sequence) capable of inhibiting leukocyte O2-
CC production. The peptides can be used as medicaments for fighting
CC infection by attracting leukocytes to a wound site and restricting tissue
CC damage at the wound site caused by excessive oxygen radicals produced by
CC these leukocytes. They can also be used to develop products for treating
CC inflammatory disease states.
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 90; DB 17; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 9
AAR94446
ID AAR94446 standard; peptide; 39 AA.
XX
AC AAR94446;
XX
DT 05-NOV-1996 (first entry)
XX
DE Synducin peptide (PR-39) induces syndecan expression.
XX
KW Synducin; induction; expression; syndecan-1; syndecan-4; surface;
KW mesenchymal cell; fibroblast; epithelial; PR-39; treatment; stasis;
KW decubitus; ulcers; keloids; skin burns; ischemic tissues;
KW hypercoagulation states; prevention; tumour metastasis; restenosis;
KW inhibition; angiogenesis; proliferation; endothelial.
XX
OS Synthetic.
XX
PN WO9609322-A2.
XX
PD 28-MAR-1996.
XX
PF 22-SEP-1995; 95WO-US12080.
XX
PR 22-SEP-1994; 94US-0310722.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Bernfield M, Gallo RL;
XX
DR WPI; 1996-188401/19.
XX
PT Modulating mesenchymal interaction by administration of synducin -
PT used in the treatment of wounds, tumours, restenosis, etc
XX
PS Claim 4; Page 26; 34pp; English.
XX
CC The present peptide is a synducin, which induces the expression of
CC syndecan-1 and syndecan-4 on the surface of mesenchymal cells, esp.
CC fibroblasts and epithelial cells. The 36 N-terminal amino acids of
CC the peptide were found to be identical to the 36 N-terminal amino
CC acids of PR-39, a Pro and Arg rich antibacterial peptide previously
CC found in porcine intestine (WO9222578). Synducins may be used in
CC the treatment of stasis and decubitus ulcers, keloids, skin burns,
CC ischemic tissues and hypercoagulation states, prevention of tumour
CC metastasis, restenosis inhibition and endothelial cell angiogenesis
CC and proliferation induction.
CC Human microvascular endothelial cells were assayed for syndecan-4
CC expression following exposure to 5 % wound fluid, dbcAMP (1 mM),
CC the present peptide (10 microM) or a blank, to give respective
CC cell surface syndecan-4 values (mOD/m in) of approx. 1.75, 1.70,
CC 1.80 and 0.95.
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 90; DB 17; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 10
AAR99121
ID AAR99121 standard; peptide; 39 AA.
XX
AC AAR99121;
XX
DT 28-OCT-1996 (first entry)
XX
DE Magainin-derived antimicrobial STD-inhibiting peptide, MSI-1312.
XX
KW STD; sexually transmitted disease; HIV; human immunodeficiency virus;
KW herpes simplex virus; HSV; Neisseria gonnorhoeae; Candida; Chlamydia;
KW magainin; antimicrobial; squalamine.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 39
FT /note= "amidated"
XX
PN WO9608270-A2.
XX
PD 21-MAR-1996.
XX
PF 13-SEP-1995; 95WO-US11675.
XX
PR 13-SEP-1994; 94US-0305475.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Bedi G, Jacob L, Williams T, Zasloff M;
XX
DR WPI; 1996-179725/18.
XX
PT Inhibiting sexually transmitted disease e.g. HIV or herpes simplex -
PT by administering magainin antimicrobial or squalamine cpd. to
PT inhibit transmission
XX
PS Example 1; Page 32; 60pp; English.
XX
CC AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may
CC be used to treat sexually transmitted diseases (STDs) caused by
CC Chlamydia, HIV, herpes simplex virus, Neisseria gonnorhoeae or
CC Candida infection. The peptides inhibit STDs by either killing the
CC infectious organism, impeding the infection mechanism or
CC interrupting the replication cycle of the organism. Squalamine (an
CC aminosterol host defence molecule of the dog fish shark Squalus
CC acanthias) and PGLa (a frog antimicrobial peptide) analogues may
CC also be useful in inhibiting STD infection and transmission.

```
XX
SQ   Sequence   39 AA;

  Query Match           100.0%;  Score 90;  DB 17;  Length 39;
  Best Local Similarity  100.0%;  Pred. No. 0.00047;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRPP 15
          |||||||||||||||
Db      1 RRRPRPPYLPRPRPP 15


RESULT 11
AAW75722
ID   AAW75722 standard; peptide; 39 AA.
XX
AC   AAW75722;
XX
DT   19-NOV-1998  (first entry)
XX
DE   Proline/Arginine rich peptide PR-39.
XX
KW   Proline; arginine; peptide; reperfusion injury; neutrophil; endothelium;
KW   superoxide; neutrophil superoxide anion; chemotaxis; NADPH oxidase;
KW   coronary bypass; organ transplantation surgery.
XX
OS   Synthetic.
XX
PN   WO9835690-A1.
XX
PD   20-AUG-1998.
XX
PF   17-FEB-1998;   98WO-US03207.
XX
PR   16-FEB-1998;   98US-0024975.
PR   18-FEB-1997;   97US-0802306.
XX
PA   (UNIV ) UNIV KANSAS STATE RES FOUND.
XX
PI   Blecha F,  Ross CR,  Shi J;
XX
DR   WPI; 1998-495359/42.
XX
PT   Reduction of reperfusion injury in temporarily occluded blood
PT   vessels  - by administration of a peptide which is rich in proline
PT   or arginine residues
XX
PS   Claim 3; Page 14; 35pp; English.
XX
CC   Sequences AAW75722-W75732 are proline/arginine rich peptides that upon
CC   administration into a mammal's bloodstream reduce reperfusion injury
CC   (production of reactive oxygen species, neutrophil adherence to
CC   endothelium, and extravasation of neutrophils). These peptides have two
CC   requirements: they contain the consensus sequence PXXP, where P is a
CC   proline residue and X is any amino acid residue, which has been found to
CC   inhibit superoxide production, and secondly they have arginine residues
CC   adjacent to these motifs, required for effective inhibition.  It was
CC   established by structural and function analysis that a peptide should
CC   ideally contain 4 or 6 of these motifs, and that inhibitory activity is
CC   correlated  with the increase of length of peptides.  The effectiveness
CC   of these peptides was determined by investigating the production of the
CC   neutrophil superoxide anion, and also the inhibition of neutrophil
CC   chemotaxis.  From this, it was found that all of the peptides inhibited
CC   NADPH oxidase to some extent.  All of the peptides also inhibit
CC   neutrophil oxidase activity.  PR-39 is believed, to be the most potent
CC   endogenous down regulator of NADPH oxidase yet discovered, and from the
CC   data produced, it can be suggested to be involved in eliminating or
CC   reducing the reperfusion injury induced adhesion and extraction of
CC   neutrophils.  The peptides are also useful in connection with surgical
CC   procedures such as coronary bypass and organ transplantation surgery.
XX
SQ   Sequence   39 AA;

  Query Match           100.0%;  Score 90;  DB 19;  Length 39;
  Best Local Similarity  100.0%;  Pred. No. 0.00047;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRPP 15
          |||||||||||||||
Db      1 RRRPRPPYLPRPRPP 15


RESULT 12
AAB26888
ID   AAB26888 standard; peptide; 39 AA.
XX
AC   AAB26888;
XX
DT   01-FEB-2001  (first entry)
XX
DE   PR-39 peptide used in angiogenesis control.
XX
KW   Angiogenesis; stimulation; PR-39; anoxia; myocardial infarction;
KW   myocardial ischaemia; proteasome.
XX
OS   Synthetic.
XX
PN   WO200057895-A1.
XX
PD   05-OCT-2000.
XX
PF   16-MAR-2000; 2000WO-US07050.
XX
PR   26-MAR-1999;   99US-0276868.
XX
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Simons M,  Gao Y;
XX
DR   WPI; 2000-628319/60.
XX
PT   Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
PT   infarction, by administering a PR-39 oligopeptide that regulates
PT   enzymatic activity of proteosomes  -
XX
PS   Disclosure; Page 21; 51pp; English.
XX
CC   This invention relates to a method for the stimulation of angiogenesis in
CC   situ within a targeted collection of viable cells. The method comprises
CC   introducing, into the cytoplasm, at least 1 member of the PR-39
CC   oligopeptide collective, which interacts with cytoplasmic proteasomes.
CC   Part of the proteolytic activity of the proteosomes is selectively
CC   altered so as to stimulate angiogenesis. The method is used to induce
CC   angiogenesis in tissue that has suffered anoxia or infarction,
CC   e.g. myocardial infarction or chronic myocardial ischaemia, and also to
CC   study the mechanisms that control angiogenesis. The present sequence
CC   represents  the PR-39 peptide from which peptide used in the method of
CC   the invention are derived.
XX
SQ   Sequence   39 AA;

  Query Match           100.0%;  Score 90;  DB 21;  Length 39;
  Best Local Similarity  100.0%;  Pred. No. 0.00047;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRPP 15
          |||||||||||||||
Db      1 RRRPRPPYLPRPRPP 15


RESULT 13
AAB84690
ID   AAB84690 standard; protein; 39 AA.
XX
AC   AAB84690;
XX
```

DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a PR-39 protein.
XX
KW PR-39; IkappaBalpha degradation; NFkappaB transcription factor;
KW myocardial infarction; chronic myocardial ischemia; heart disease;
KW anoxia.
XX
OS Unidentified.
XX
PN WO200147540-A1.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-US35293.
XX
PR 29-DEC-1999; 99US-0474967.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2001-441690/47.
XX
PT Selective inhibition of IkappaBalpha degradation within targeted viable
PT cell collection, involves interacting PR-39 oligopeptide with
PT IkappaBalpha and proteasomes, and altering proteolytic activity of
PT proteasomes -
XX
PS Disclosure; Page 30; 69pp; English.
XX
CC The present sequence represents a PR-39 protein. The specification
CC describes PR-39 derived peptides, which are used for selective
CC inhibition of IkappaBalpha degradation within a targeted cell collection
CC in-situ. The method is useful for selectively inhibiting IkappaBalpha
CC protein degradation in situ, decreasing the activity of NFkappaB
CC transcription factor and selective control of NFkappaB-dependent gene
CC expression in situ. The PR-39 derived peptides are useful in the
CC treatment of myocardial infarction, chronic myocardial ischemia of
CC heart disease and anoxia.
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 90; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 14
AAB97280
ID AAB97280 standard; peptide; 39 AA.
XX
AC AAB97280;
XX
DT 09-AUG-2001 (first entry)
XX
DE PR-39 peptide.
XX
KW PR-39; cathelin; inflammation; wound healing; myocardial infarction;
KW proteasome; proteolysis; alpha7; peptide degradation; angiogenesis;
KW anoxia; chronic myocardial ischaemia; heart tissue.
XX
OS Unidentified.
XX
PN WO200130368-A1.
XX
PD 03-MAY-2001.
XX
PF 06-OCT-2000; 2000WO-US27552.
XX
PR 25-OCT-1999; 99US-0426011.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Simons M, Gao Y;
XX
DR WPI; 2001-355179/37.
XX
PT Stimulation of angiogenesis and inhibition of proteasome mediated
PT degradation in cells, by introduction of PR-39 oligopeptide or its
PT N-terminal fragments or their conjugates, for use in anoxia and
PT infarction conditions -
XX
PS Disclosure; Page 21; 52pp; English.
XX
CC Peptides AAB97277 - AAB97279 represent PR-39 derived oligopeptides. PR-39
CC is a member of the the cathelin family of proteins, mature PR-39
CC represented by the present sequence is 39 amino acids in length, and has
CC been shown to play a role in several inflammatory events including wound
CC healing and myocardial infarction. The PR-39 derived family of
CC oligopeptides cause selective inhibition of proteasome mediated
CC degeneration of peptides and stimulation of angiogenesis after their
CC intracellular introduction to a target cell. PR-39 derived peptides are
CC able to interact with at least the alpha7 subunit of the proteasomes, and
CC therefore alter the proteolytic activity of proteasomes such that a
CC selective increased expression of specific proteins occurs. The invention
CC includes methods for the selective inhibition of proteasome mediated
CC peptide degradation. The method provides means for stimulating
CC angiogenesis as required in living tissues and organs which have suffered
CC defects or have undergone anoxia and/or infarction, myocardial infarction
CC or chronic myocardial ischaemia of heart tissue. Examples are the
CC myocardium, skeletal or smooth muscle, artery or vein, lung, brain,
CC kidney, spleen, liver, gastrointestinal or nerve tissues, limbs, and
CC extremities. A particular example is after myocardial infarction or
CC ischaemia.
XX
SQ Sequence 39 AA;

Query Match 100.0%; Score 90; DB 22; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15
||||||||||||||||
Db 1 RRRPRPPYLPRPRPP 15

RESULT 15
ABB07714
ID ABB07714 standard; peptide; 42 AA.
XX
AC ABB07714;
XX
DT 10-JUN-2002 (first entry)
XX
DE Antimicrobial peptide PR-39 C-terminal fragment.
XX
KW Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response;
KW antigen presenting cell; adjuvant; porcine; PR-39.
XX
OS Sus sp.
XX
PN WO200213857-A2.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-EP09529.
XX
PR 17-AUG-2000; 2000AT-0001416.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX

PI Fritz J, Mattner F, Zauner W, Buschle M, Egyed A;
XX
DR WPI; 2002-269154/31.
XX
PT Vaccine for active immunization or for preparing an adjuvant for
PT enhancing an immune response to at least one antigen, comprises at
PT least one antigen and at least one cathelicidin derived antimicrobial
PT peptide -
XX
PS Disclosure; Fig 3; 65pp; English.
XX
CC The invention relates to a vaccine comprising at least one antigen and at
CC least one cathelicidin derived antimicrobial peptide or its derivative.
CC The vaccine is useful for active immunization, especially of humans or
CC animals without protection against the specific antigen. The cathelicidin
CC derived antimicrobial peptide is useful in the preparation of an adjuvant
CC for enhancing the immune response to at least one antigen, where the
CC adjuvant enhances the uptake of at least one antigen in antigen
CC presenting cells (APC), and the adjuvant is added to the vaccine.
CC Sequences ABB07708-15 represent C-terminal fragments of antimicrobial
CC peptides of the cathelicicidin family.
XX
SQ Sequence 42 AA;

Query Match 100.0%; Score 90; DB 23; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 RRRPRPPYLPRPRPP 15
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Db       1 RRRPRPPYLPRPRPP 15
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Job time : 36 secs

OM protein - protein search, using sw model

Run on: May 13, 2003, 10:40:17 ; Search time 14 Seconds
(without alignments)
31.525 Million cell updates/sec

Title: US-09-426-011D-3
Perfect score: 90
Sequence: 1 RRRPRPPYLPRPRPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	26	2	US-08-419-066-2	Sequence 2, Appli
2	90	100.0	26	4	US-09-024-975-2	Sequence 2, Appli
3	90	100.0	39	1	US-08-162-052-1	Sequence 1, Appli
4	90	100.0	39	1	US-08-310-722-1	Sequence 1, Appli
5	90	100.0	39	2	US-08-419-066-1	Sequence 1, Appli
6	90	100.0	39	2	US-08-728-333-1	Sequence 1, Appli
7	90	100.0	39	4	US-09-024-975-1	Sequence 1, Appli
8	90	100.0	39	5	PCT-US95-12080-1	Sequence 1, Appli
9	83	92.2	14	4	US-09-024-975-4	Sequence 4, Appli
10	66	73.3	20	4	US-09-024-975-9	Sequence 9, Appli
11	61	67.8	336	1	US-08-414-926A-26	Sequence 26, Appl
12	61	67.8	336	2	US-08-926-922-26	Sequence 26, Appl
13	61	67.8	336	3	US-09-253-682-26	Sequence 26, Appl
14	61	67.8	336	4	US-09-527-657-26	Sequence 26, Appl
15	59	65.6	59	5	PCT-US95-12080-3	Sequence 3, Appli
16	53	58.9	18	1	US-08-205-938A-23	Sequence 23, Appl
17	53	58.9	18	1	US-08-205-938A-24	Sequence 24, Appl
18	53	58.9	18	4	US-09-230-180-20	Sequence 20, Appl
19	53	58.9	18	5	PCT-US95-02626-23	Sequence 23, Appl
20	53	58.9	18	5	PCT-US95-02626-24	Sequence 24, Appl
21	52	57.8	18	1	US-08-205-938A-25	Sequence 25, Appl
22	52	57.8	18	5	PCT-US95-02626-25	Sequence 25, Appl
23	51.5	57.2	355	4	US-08-483-533-41	Sequence 41, Appl
24	51.5	57.2	355	4	US-09-283-471A-41	Sequence 41, Appl
25	51.5	57.2	355	5	PCT-US91-06532-3	Sequence 3, Appli
26	51	56.7	16	1	US-08-205-938A-8	Sequence 8, Appli
27	51	56.7	16	5	PCT-US95-02626-8	Sequence 8, Appli
28	51	56.7	180	3	US-09-187-331-5	Sequence 5, Appli
29	51	56.7	180	4	US-09-470-946-5	Sequence 5, Appli
30	51	56.7	195	3	US-09-187-331-1	Sequence 1, Appli
31	51	56.7	195	4	US-09-470-946-1	Sequence 1, Appli
32	50.5	56.1	169	4	US-08-483-533-28	Sequence 28, Appl
33	50.5	56.1	169	4	US-09-283-471A-28	Sequence 28, Appl
34	50.5	56.1	393	4	US-09-432-470-2	Sequence 2, Appli
35	50.5	56.1	393	4	US-09-432-470-4	Sequence 4, Appli
36	50	55.6	16	1	US-08-205-938A-7	Sequence 7, Appli
37	50	55.6	16	1	US-08-205-938A-28	Sequence 28, Appl
38	50	55.6	16	5	PCT-US95-02626-7	Sequence 7, Appli
39	50	55.6	16	5	PCT-US95-02626-28	Sequence 28, Appl
40	50	55.6	17	1	US-08-205-938A-27	Sequence 27, Appl
41	50	55.6	17	5	PCT-US95-02626-27	Sequence 27, Appl
42	49.5	55.0	129	4	US-09-199-637A-97	Sequence 97, Appl
43	49	54.4	26	4	US-09-024-975-8	Sequence 8, Appli
44	48.5	53.9	716	4	US-09-186-276B-67	Sequence 67, Appl
45	48.5	53.9	716	4	US-08-842-445-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-08-419-066-2
; Sequence 2, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match 100.0%; Score 90; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRPRPPYLPRPRPP 15

```
          ||||||||||||||||
Db      1 RRRPRPPYLPRPRPP 15


RESULT 2
US-09-024-975-2
; Sequence 2, Application US/09024975
; Patent No. 6133233
;  GENERAL INFORMATION:
;    APPLICANT:  ROSS, CHRISTOPHER R.
;    APPLICANT:  BLECHA, FRANK
;    APPLICANT:  SHI, JISHU
;    TITLE OF INVENTION:  PEPTIDE MODULATION OF REPERFUSION INJURY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MO
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,975
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/802,306
;      FILING DATE:  18-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M.
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  25585-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-975-2

  Query Match             100.0%;  Score 90;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRPP 15
          ||||||||||||||||
Db      1 RRRPRPPYLPRPRPP 15


RESULT 3
US-08-162-052-1
; Sequence 1, Application US/08162052
; Patent No. 5489575
;  GENERAL INFORMATION:
;    APPLICANT:  LEE, Jong-Youn
;    APPLICANT:  BOMAN, Hans G
;    APPLICANT:  MUTT, Viktor
;    APPLICANT:  JORNVALL, Hans
;    TITLE OF INVENTION:  NOVEL POLYPEPTIDES AND THEIR USE
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/162,052
;      FILING DATE:  02-JUN-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9101838-2
;      FILING DATE:  14-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO 92-22578
;      FILING DATE:  23-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crane-Feury, Sharon E
;      REGISTRATION NUMBER:  36,113
;      REFERENCE/DOCKET NUMBER:  003300-299
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-162-052-1

  Query Match             100.0%;  Score 90;  DB 1;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRPP 15
          ||||||||||||||||
Db      1 RRRPRPPYLPRPRPP 15


RESULT 4
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
;  GENERAL INFORMATION:
;    APPLICANT:  Gallo, Richard L.
;    APPLICANT:  Klagsbrun, Michael
;    TITLE OF INVENTION:  Synducin Mediated Modulation of Tissue Repair
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/310,722
;      FILING DATE:  22-SEP-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  CMCC379
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404)-815-6508
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;       TELEFAX:  (404)-815-6555
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lee, Jong-Youn
;      AUTHORS:  Boman, Hans G.
;      AUTHORS:  Mutt, Viktor
;      AUTHORS:  Jornvall, Hans
;      TITLE:  No. 5654273el Polypeptides And Their Use
;      JOURNAL:  PCT WO 92/22578
;      DATE:  12/23/92
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 39
US-08-310-722-1

  Query Match             100.0%;  Score 90;  DB 1;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           |||||||||||||||
Db       1 RRRPRPPYLPRPRPP 15


RESULT 5
US-08-419-066-1
; Sequence 1, Application US/08419066
; Patent No. 5830993
;  GENERAL INFORMATION:
;    APPLICANT:  Blecha, Frank
;    APPLICANT:  Shi, Jishu
;    TITLE OF INVENTION:  SYNTHETIC ANTIMICROBIAL PEPTIDE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John M. Collins,  Hovey, Williams, Timmons &
;      ADDRESSEE:  Collins
;      STREET:  2405 Grand Boulevard, Suite 400
;      CITY:  Kansas City
;      STATE:  Missouri
;      COUNTRY:  U.S.A.
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,066
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Collins, John M.
;      REGISTRATION NUMBER:  26262
;      REFERENCE/DOCKET NUMBER:  23625
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (816) 474-9050
;      TELEFAX:  (816) 474-9057
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-419-066-1

  Query Match             100.0%;  Score 90;  DB 2;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           |||||||||||||||
Db       1 RRRPRPPYLPRPRPP 15


RESULT 6
US-08-728-333-1
; Sequence 1, Application US/08728333
; Patent No. 5863897
;  GENERAL INFORMATION:
;    APPLICANT:  Gallo, Richard L.
;    APPLICANT:  Klagsbrun, Michael
;    TITLE OF INVENTION:  Synducin Mediated Modulation of Tissue Repair
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/728,333
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/310,722
;      FILING DATE:  22-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  CMCC379
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404)-815-6508
;      TELEFAX:  (404)-815-6555
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lee, Jong-Youn
;      AUTHORS:  Boman, Hans G.
;      AUTHORS:  Mutt, Viktor
;      AUTHORS:  Jornvall, Hans
;      TITLE:  No. 5863897el Polypeptides And Their Use
;      JOURNAL:  PCT WO 92/22578
;      DATE:  12/23/92
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 39
US-08-728-333-1

  Query Match             100.0%;  Score 90;  DB 2;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           |||||||||||||||
Db       1 RRRPRPPYLPRPRPP 15
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RESULT 7
US-09-024-975-1
; Sequence 1, Application US/09024975
; Patent No. 6133233
;  GENERAL INFORMATION:
;    APPLICANT:  ROSS, CHRISTOPHER R.
;    APPLICANT:  BLECHA, FRANK
;    APPLICANT:  SHI, JISHU
;    TITLE OF INVENTION:  PEPTIDE MODULATION OF REPERFUSION INJURY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MO
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,975
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/802,306
;      FILING DATE:  18-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M.
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  25585-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-975-1

  Query Match             100.0%;  Score 90;  DB 4;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           |||||||||||||||
Db       1 RRRPRPPYLPRPRPP 15


RESULT 8
PCT-US95-12080-1
; Sequence 1, Application PC/TUS9512080
;  GENERAL INFORMATION:
;    APPLICANT:  Children's Medical Center Corporaton
;    TITLE OF INVENTION:  Synducin Mediated Modulation of Tissue Repair
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12080
;      FILING DATE:
;      CLASSIFICATION:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404)-873-8794
;      TELEFAX:  (404)-815-8795
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  39 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lee, Jong-Youn
;      AUTHORS:  Boman, Hans G.
;      AUTHORS:  Mutt, Viktor
;      AUTHORS:  Jornvall, Hans
;      TITLE:  Novel Polypeptides And Their Use
;      JOURNAL:  PCT WO 92/22578
;      DATE:  12/23/92
;      RELEVANT RESIDUES IN SEQ ID NO:  1: FROM 1 TO 39
PCT-US95-12080-1

  Query Match             100.0%;  Score 90;  DB 5;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           |||||||||||||||
Db       1 RRRPRPPYLPRPRPP 15


RESULT 9
US-09-024-975-4
; Sequence 4, Application US/09024975
; Patent No. 6133233
;  GENERAL INFORMATION:
;    APPLICANT:  ROSS, CHRISTOPHER R.
;    APPLICANT:  BLECHA, FRANK
;    APPLICANT:  SHI, JISHU
;    TITLE OF INVENTION:  PEPTIDE MODULATION OF REPERFUSION INJURY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MO
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,975
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/802,306
;      FILING DATE:  18-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M.
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  25585-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-975-4

  Query Match             92.2%;  Score 83;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0.00023;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRP 14
          ||||||||||||||
Db      1 RRRPRPPYLPRPRP 14


RESULT 10
US-09-024-975-9
; Sequence 9, Application US/09024975
; Patent No. 6133233
;  GENERAL INFORMATION:
;    APPLICANT:  ROSS, CHRISTOPHER R.
;    APPLICANT:  BLECHA, FRANK
;    APPLICANT:  SHI, JISHU
;    TITLE OF INVENTION:  PEPTIDE MODULATION OF REPERFUSION INJURY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HOVEY, WILLIAMS, TIMMONS & COLLINS
;      STREET:  2405 GRAND BLVD., SUITE 400
;      CITY:  KANSAS CITY
;      STATE:  MO
;      COUNTRY:  USA
;      ZIP:  64108
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/024,975
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/802,306
;      FILING DATE:  18-FEB-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  COLLINS, JOHN M.
;      REGISTRATION NUMBER:  26,262
;      REFERENCE/DOCKET NUMBER:  25585-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  816/474-9050
;      TELEFAX:  816/474-9057
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-024-975-9

  Query Match             73.3%;  Score 66;  DB 4;  Length 20;
  Best Local Similarity   85.7%;  Pred. No. 0.032;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRP 14
          | ||||| ||||||
Db      2 RIRPRPPRLPRPRP 15


RESULT 11
US-08-414-926A-26
; Sequence 26, Application US/08414926A
; Patent No. 5721354
;  GENERAL INFORMATION:
;    APPLICANT:  Spaete, Richard
;    APPLICANT:  Cha, Tai-An
;    TITLE OF INVENTION:  NOVEL HUMAN CYTOMEGALOVIRUS
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/414,926A
;      FILING DATE:  March 31, 1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  AVIR-011/OOUS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-494-7622
;      TELEFAX:  415-857-0663
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    IMMEDIATE SOURCE:
;      CLONE:  tol.22
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..336
;      OTHER INFORMATION:  /label= UL151
US-08-414-926A-26

  Query Match             67.8%;  Score 61;  DB 1;  Length 336;
  Best Local Similarity   78.6%;  Pred. No. 1.7;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 RRPRPPYLPRPRPP 15
          ||| || | |||||
Db    279 RRPIPPILQRPRPP 292


RESULT 12
US-08-926-922-26
; Sequence 26, Application US/08926922
; Patent No. 5925751
;  GENERAL INFORMATION:
;    APPLICANT:  Spaete, Richard
;    APPLICANT:  Cha, Tai-An
;    TITLE OF INVENTION:  NOVEL HUMAN CYTOMEGALOVIRUS
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Luann Cserr Attorney at Law
;      STREET:  750 Arimo Avenue
;      CITY:  Oakland
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/926,922
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;      FILING DATE:  September 10, 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  AVIR 11A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-834-1448
;      TELEFAX:  510-839-7810
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    IMMEDIATE SOURCE:
;      CLONE:  tol.22
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..336
;      OTHER INFORMATION:  /label= UL151
US-08-926-922-26

  Query Match             67.8%;  Score 61;  DB 2;  Length 336;
  Best Local Similarity   78.6%;  Pred. No. 1.7;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 RRPRPPYLPRPRPP 15
           ||| || | |||||
Db     279 RRPIPPILQRPRPP 292


RESULT 13
US-09-253-682-26
; Sequence 26, Application US/09253682
; Patent No. 6040170
;  GENERAL INFORMATION:
;    APPLICANT:  Spaete, Richard
;    APPLICANT:  Cha, Tai-An
;    TITLE OF INVENTION:  NOVEL HUMAN CYTOMEGALOVIRUS
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Luann Cserr Attorney at Law
;      STREET:  750 Arimo Avenue
;      CITY:  Oakland
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94610
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/253,682
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/926,922
;      FILING DATE:  September 10, 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  AVIR 11A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-834-1448
;      TELEFAX:  510-839-7810
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    IMMEDIATE SOURCE:
;      CLONE:  tol.22
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..336
;      OTHER INFORMATION:  /label= UL151
US-09-253-682-26

  Query Match             67.8%;  Score 61;  DB 3;  Length 336;
  Best Local Similarity   78.6%;  Pred. No. 1.7;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 RRPRPPYLPRPRPP 15
           ||| || | |||||
Db     279 RRPIPPILQRPRPP 292


RESULT 14
US-09-527-657-26
; Sequence 26, Application US/09527657
; Patent No. 6291236
;  GENERAL INFORMATION:
;       APPLICANT: Spaete, Richard
;                  Cha, Tai-An
;       TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
;       NUMBER OF SEQUENCES: 27
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Luann Cserr Attorney at Law
;            STREET: 750 Arimo Avenue
;            CITY: Oakland
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94610
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/527,657
;            FILING DATE: 17-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/926,922
;            FILING DATE: September 10, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: AVIR 11A
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 510-834-1448
;            TELEFAX: 510-839-7810
;   INFORMATION FOR SEQ ID NO: 26:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 336 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       IMMEDIATE SOURCE:
;            CLONE: tol.22
;       FEATURE:
;            NAME/KEY:  Protein
;            LOCATION:  1..336
;            OTHER INFORMATION:  /label= UL151
;       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-527-657-26

  Query Match             67.8%;  Score 61;  DB 4;  Length 336;
  Best Local Similarity   78.6%;  Pred. No. 1.7;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 RRPRPPYLPRPRPP 15
           ||| || | |||||
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```
Db    279 RRPIPPILQRPRPP 292


RESULT 15
PCT-US95-12080-3
; Sequence 3, Application PC/TUS9512080
;  GENERAL INFORMATION:
;    APPLICANT:  Children's Medical Center Corporaton
;    TITLE OF INVENTION:  Synducin Mediated Modulation of Tissue Repair
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12080
;      FILING DATE:
;      CLASSIFICATION:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404)-873-8794
;      TELEFAX:  (404)-815-8795
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  59 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
PCT-US95-12080-3

  Query Match             65.6%;  Score 59;  DB 5;  Length 59;
  Best Local Similarity   84.6%;  Pred. No. 0.57;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPR 13
           | ||||| |||||
Db       2 RIRPRPPRLPRPR 14


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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

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Title: US-09-426-011D-3
Perfect score: 90
Sequence: 1 RRRPRPPYLPRPRPP 15

Scoring table: BLOSUM62
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Searched: 349150 seqs, 92025710 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	60	66.7	953	10	US-09-888-615-66	Sequence 66, Appl
3	56.5	62.8	74	10	US-09-864-761-45555	Sequence 45555, A
4	55	61.1	45	10	US-09-864-761-49065	Sequence 49065, A
5	54	60.0	250	9	US-10-102-806-517	Sequence 517, App
6	53	58.9	18	10	US-09-030-619-96	Sequence 96, Appl
7	53	58.9	18	10	US-09-030-619-158	Sequence 158, App
8	53	58.9	18	10	US-09-030-619-159	Sequence 159, App
9	52	57.8	18	10	US-09-030-619-160	Sequence 160, App
10	52	57.8	354	9	US-10-004-717-2	Sequence 2, Appli
11	52	57.8	354	9	US-10-004-717-58	Sequence 58, Appl
12	51	56.7	180	10	US-09-997-701-5	Sequence 5, Appli
13	51	56.7	195	10	US-09-997-701-1	Sequence 1, Appli
14	50.5	56.1	392	10	US-09-747-835A-55	Sequence 55, Appl
15	50.5	56.1	393	9	US-10-243-035-2	Sequence 2, Appli
16	50.5	56.1	419	10	US-09-828-035-2	Sequence 2, Appli
17	50.5	56.1	1314	10	US-09-747-835A-29	Sequence 29, Appl
18	50	55.6	99	10	US-09-864-761-43778	Sequence 43778, A
19	50	55.6	146	9	US-09-989-920-237	Sequence 237, App
20	50	55.6	449	9	US-10-125-540-320	Sequence 320, App
21	50	55.6	449	9	US-10-103-313-438	Sequence 438, App
22	50	55.6	449	10	US-09-764-870-320	Sequence 320, App
23	50	55.6	449	10	US-09-764-853-643	Sequence 643, App
24	49.5	55.0	129	9	US-09-975-719-97	Sequence 97, Appl
25	49	54.4	223	12	US-10-062-254-204	Sequence 204, App
26	48.5	53.9	111	10	US-09-864-761-47005	Sequence 47005, A
27	48	53.3	281	8	US-08-971-317A-6	Sequence 6, Appli
28	48	53.3	281	9	US-09-131-237-6	Sequence 6, Appli
29	48	53.3	281	9	US-10-174-654-10	Sequence 10, Appl
30	48	53.3	281	9	US-10-151-882-44	Sequence 44, Appl
31	48	53.3	281	10	US-09-802-669-25	Sequence 25, Appl
32	48	53.3	281	10	US-09-193-663-6	Sequence 6, Appli
33	48	53.3	281	10	US-09-027-287-6	Sequence 6, Appli
34	48	53.3	281	10	US-09-252-656B-6	Sequence 6, Appli
35	48	53.3	281	10	US-09-929-493-6	Sequence 6, Appli
36	48	53.3	281	10	US-09-927-110-1	Sequence 1, Appli
37	48	53.3	281	12	US-10-012-452-13	Sequence 13, Appl
38	48	53.3	1134	9	US-10-001-873-50	Sequence 50, Appl
39	47.5	52.8	272	10	US-09-925-300-1697	Sequence 1697, Ap
40	47	52.2	42	10	US-09-030-619-162	Sequence 162, App
41	47	52.2	84	9	US-10-174-590-486	Sequence 486, App
42	47	52.2	84	9	US-10-176-758-486	Sequence 486, App
43	47	52.2	84	9	US-10-175-737-486	Sequence 486, App
44	47	52.2	84	9	US-10-173-706-486	Sequence 486, App
45	47	52.2	84	9	US-10-175-738-486	Sequence 486, App

ALIGNMENTS

RESULT 1
US-09-030-619-163
; Sequence 163, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-030-619-163

Query Match 73.3%; Score 66; DB 10; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 RRRPRPPYLPRPRP 14
          | ||||| ||||||
Db      2 RIRPRPPRLPRPRP 15
```

RESULT 2
US-09-888-615-66
; Sequence 66, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN

```
;  APPLICANT:  CHARYDCZAK, GLEN
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  TITLE OF INVENTION: NOVEL PROTEASES
;  FILE REFERENCE: 038602/1214
;  CURRENT APPLICATION NUMBER: US/09/888,615
;  CURRENT FILING DATE:  2001-06-26
;  PRIOR APPLICATION NUMBER: 60/214,047
;  PRIOR FILING DATE: 2000-06-26
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-888-615-66

  Query Match             66.7%;  Score 60;  DB 10;  Length 953;
  Best Local Similarity   56.5%;  Pred. No. 17;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    8;  Gaps    1;

Qy       1 RRRPRP--------PYLPRPRPP 15
           ||||||        |  ||||||
Db     377 RRRPRPRPQTRLRTPPQPRPRPP 399


RESULT 3
US-09-864-761-45555
; Sequence 45555, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45555
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC010458.2
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =   1
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.9
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.79
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
;   OTHER INFORMATION: EST_HUMAN HIT: AW583858.1, EVALUE 5.00e-20
US-09-864-761-45555

  Query Match             62.8%;  Score 56.5;  DB 10;  Length 74;
  Best Local Similarity   56.2%;  Pred. No. 3.9;
  Matches    9;  Conservative    4;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1 RRRPRPPY-LPRPRPP 15
           || |:||: :| |:||
Db      37 RREPKPPHRIPEPKPP 52


RESULT 4
US-09-864-761-49065
; Sequence 49065, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 49065
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC005973.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.88
;   OTHER INFORMATION: EST_HUMAN HIT: AI358103.1, EVALUE 4.60e+00
US-09-864-761-49065

  Query Match             61.1%;  Score 55;  DB 10;  Length 45;
  Best Local Similarity   76.9%;  Pred. No. 3.6;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPR 13
           |||||||  |||:
Db      19 RRRPRPPGPPRPQ 31


RESULT 5
US-10-102-806-517
; Sequence 517, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA103P1C1
;  CURRENT APPLICATION NUMBER: US/10/102,806
;  CURRENT FILING DATE:  2002-03-22
;  PRIOR APPLICATION NUMBER: 09/925,298
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05881
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 846
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 517
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (118)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (161)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (204)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-517

  Query Match             60.0%;  Score 54;  DB 9;  Length 250;
  Best Local Similarity   71.4%;  Pred. No. 23;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRP 14
           ||  |||  |||||
Db     202 RRXHRPPAAPRPRP 215


RESULT 6
US-09-030-619-96
; Sequence 96, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
;  APPLICANT:  Krieger, Timothy J.
;  APPLICANT:  Taylor, Robert
;  APPLICANT:  Erfle, Douglas
;  APPLICANT:  Fraser, Janet R.
;  APPLICANT:  West, Michael H.P.
;  APPLICANT:  McNicol, Patricia J.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;  TITLE OF INVENTION:  WITH ANTIBIOTICS
;  FILE REFERENCE:  660081.406
;  CURRENT APPLICATION NUMBER: US/09/030,619B
;  CURRENT FILING DATE:  1998-02-25
;  NUMBER OF SEQ ID NOS:  232
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 96
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Cationic Peptide Analogue
US-09-030-619-96

  Query Match             58.9%;  Score 53;  DB 10;  Length 18;
  Best Local Similarity   72.7%;  Pred. No. 2.6;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 RPPYLPRPRPP 15
           || |:|:||||
Db       4 RPVYIPQPRPP 14


RESULT 7
US-09-030-619-158
; Sequence 158, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
;  APPLICANT:  Krieger, Timothy J.
;  APPLICANT:  Taylor, Robert
;  APPLICANT:  Erfle, Douglas
;  APPLICANT:  Fraser, Janet R.
;  APPLICANT:  West, Michael H.P.
;  APPLICANT:  McNicol, Patricia J.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;  TITLE OF INVENTION:  WITH ANTIBIOTICS
;  FILE REFERENCE:  660081.406
;  CURRENT APPLICATION NUMBER: US/09/030,619B
;  CURRENT FILING DATE:  1998-02-25
;  NUMBER OF SEQ ID NOS:  232
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 158
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Apis mellifera
US-09-030-619-158

  Query Match             58.9%;  Score 53;  DB 10;  Length 18;
  Best Local Similarity   72.7%;  Pred. No. 2.6;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 RPPYLPRPRPP 15
           || |:|:||||
Db       4 RPVYIPQPRPP 14


RESULT 8
US-09-030-619-159
; Sequence 159, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
;  APPLICANT:  Krieger, Timothy J.
```

```
;  APPLICANT:  Taylor, Robert
;  APPLICANT:  Erfle, Douglas
;  APPLICANT:  Fraser, Janet R.
;  APPLICANT:  West, Michael H.P.
;  APPLICANT:  McNicol, Patricia J.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;  TITLE OF INVENTION:  WITH ANTIBIOTICS
;  FILE REFERENCE:  660081.406
;  CURRENT APPLICATION NUMBER: US/09/030,619B
;  CURRENT FILING DATE:  1998-02-25
;  NUMBER OF SEQ ID NOS:  232
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 159
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Apis mellifera
US-09-030-619-159

  Query Match             58.9%;  Score 53;  DB 10;  Length 18;
  Best Local Similarity   72.7%;  Pred. No. 2.6;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 RPPYLPRPRPP 15
           || |:|:|||| 
Db       4 RPVYIPQPRPP 14


RESULT 9
US-09-030-619-160
; Sequence 160, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
;  APPLICANT:  Krieger, Timothy J.
;  APPLICANT:  Taylor, Robert
;  APPLICANT:  Erfle, Douglas
;  APPLICANT:  Fraser, Janet R.
;  APPLICANT:  West, Michael H.P.
;  APPLICANT:  McNicol, Patricia J.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;  TITLE OF INVENTION:  WITH ANTIBIOTICS
;  FILE REFERENCE:  660081.406
;  CURRENT APPLICATION NUMBER: US/09/030,619B
;  CURRENT FILING DATE:  1998-02-25
;  NUMBER OF SEQ ID NOS:  232
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 160
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Apis mellifera
US-09-030-619-160

  Query Match             57.8%;  Score 52;  DB 10;  Length 18;
  Best Local Similarity   72.7%;  Pred. No. 3.3;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 RPPYLPRPRPP 15
           || |:|:|||| 
Db       4 RPIYIPQPRPP 14


RESULT 10
US-10-004-717-2
; Sequence 2, Application US/10004717
; Publication No. US20020192665A1
; GENERAL INFORMATION:
;  APPLICANT: ZOGHBI, HUDA Y.
;  APPLICANT:  YANG, QI
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN
;  TITLE OF INVENTION:  ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
;  TITLE OF INVENTION:  OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
;  FILE REFERENCE: P01899US4
;  CURRENT APPLICATION NUMBER: US/10/004,717
;  CURRENT FILING DATE:  2002-08-16
;  PRIOR APPLICATION NUMBER: 09/585,645
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 60/176,993
;  PRIOR FILING DATE: 2000-01-19
;  PRIOR APPLICATION NUMBER: 60/137,060
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-004-717-2

  Query Match             57.8%;  Score 52;  DB 9;  Length 354;
  Best Local Similarity   57.1%;  Pred. No. 52;
  Matches    8;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 RRPRPPYLPRPRPP 15
           |:|:| :||:| || 
Db      21 RQPQPHHLPQPPPP 34


RESULT 11
US-10-004-717-58
; Sequence 58, Application US/10004717
; Publication No. US20020192665A1
; GENERAL INFORMATION:
;  APPLICANT: ZOGHBI, HUDA Y.
;  APPLICANT:  YANG, QI
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN
;  TITLE OF INVENTION:  ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
;  TITLE OF INVENTION:  OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
;  FILE REFERENCE: P01899US4
;  CURRENT APPLICATION NUMBER: US/10/004,717
;  CURRENT FILING DATE:  2002-08-16
;  PRIOR APPLICATION NUMBER: 09/585,645
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 60/176,993
;  PRIOR FILING DATE: 2000-01-19
;  PRIOR APPLICATION NUMBER: 60/137,060
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 354
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-004-717-58

  Query Match             57.8%;  Score 52;  DB 9;  Length 354;
  Best Local Similarity   57.1%;  Pred. No. 52;
  Matches    8;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 RRPRPPYLPRPRPP 15
           |:|:| :||:| || 
Db      21 RQPQPHHLPQPPPP 34


RESULT 12
US-09-997-701-5
; Sequence 5, Application US/09997701
; Patent No. US20020107180A1
; GENERAL INFORMATION:
;  APPLICANT: Yue, Henry
;  APPLICANT:  Corley, Neil C.
;  APPLICANT:  Guegler, Karl J.
;  APPLICANT:  Gorgone, Gina A.
;  APPLICANT:  Baughn, Mariah R.
;  TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
;  FILE REFERENCE: PF-0631 US
```

; CURRENT APPLICATION NUMBER: US/09/997,701
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/470,946
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: g2499136
US-09-997-701-5

Query Match 56.7%; Score 51; DB 10; Length 180;
Best Local Similarity 53.8%; Pred. No. 36;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RPRPPYLPRPRPP 15
:|:||| |:| |
Db 47 KPKPPYYPQPENP 59

RESULT 13
US-09-997-701-1
; Sequence 1, Application US/09997701
; Patent No. US20020107180A1
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina A.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
; FILE REFERENCE: PF-0631 US
; CURRENT APPLICATION NUMBER: US/09/997,701
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/470,946
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2297891
US-09-997-701-1

Query Match 56.7%; Score 51; DB 10; Length 195;
Best Local Similarity 53.8%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RPRPPYLPRPRPP 15
:|:||| |:| |
Db 47 KPKPPYYPQPENP 59

RESULT 14
US-09-747-835A-55
; Sequence 55, Application US/09747835A
; Patent No. US20020146692A1
; GENERAL INFORMATION:
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Wang, Dunrui
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Asundi, Vinod
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE

; TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: HYS-37CIP
; CURRENT APPLICATION NUMBER: US/09/747,835A
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 09/729,739
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-835A-55

Query Match 56.1%; Score 50.5; DB 10; Length 392;
Best Local Similarity 68.8%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 RRRPRPPYLP-RPRPP 15
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Db 368 RRRPNPPRKPVRPRGP 383

RESULT 15
US-10-243-035-2
; Sequence 2, Application US/10243035
; Publication No. US20030049697A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: MAINGRET, FRANCOIS
; TITLE OF INVENTION: NEW FAMILY OF MECHANOSENSITIVE HUMAN POTASSIUM CHANNELS
; TITLE OF INVENTION: ACTIVATED BY POLYUNSATURATED FATTY ACIDS AND THEIR USE
; FILE REFERENCE: 1317-02
; CURRENT APPLICATION NUMBER: US/10/243,035
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-035-2

Query Match 56.1%; Score 50.5; DB 9; Length 393;
Best Local Similarity 68.8%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 1 RRRPRPPYLP-RPRPP 15
|||| || | ||| |
Db 368 RRRPNPPRKPVRPRGP 383

Search completed: May 13, 2003, 10:42:32
Job time : 18 secs

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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 13, 2003, 10:38:17 ; Search time 16 Seconds
(without alignments)
90.126 Million cell updates/sec

Title: US-09-426-011D-3
Perfect score: 90
Sequence: 1 RRRPRPPYLPRPRPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	172	2	S68232	antimicrobial prot
2	66	73.3	59	2	A36589	bactenecin 7 - bov
3	59.5	66.1	82	2	A41051	spore coat protein
4	58	64.4	190	2	S68230	antimicrobial pept
5	56.5	62.8	168	2	S35330	apidaecin 14 precu
6	56.5	62.8	199	2	S14981	extensin class I (
7	55	61.1	437	2	A88942	protein R13D11.3 [
8	54.5	60.6	301	2	JQ1663	hybrid proline-ric
9	54	60.0	359	2	T13478	hypothetical prote
10	54	60.0	427	2	T32652	hypothetical prote
11	53	58.9	26	2	S06675	apidaecin Ib precu
12	53	58.9	144	2	S35331	apidaecin 22 precu
13	53	58.9	184	2	T29373	hypothetical prote
14	53	58.9	283	2	S35332	apidaecin 73 precu
15	53	58.9	428	2	E71415	probable coll wall
16	53	58.9	491	2	T07598	proline-rich prote
17	52	57.8	261	1	WMBEXE	infected cell prot
18	52	57.8	439	2	S51939	chitinase (EC 3.2.
19	52	57.8	467	2	S71169	protein kinase, 54
20	52	57.8	1006	2	G86292	hypothetical prote
21	51.5	57.2	1187	1	JC4155	protein-tyrosine-p
22	51.5	57.2	1189	1	JC2366	protein-tyrosine-p
23	51	56.7	180	2	S43791	PBDX protein - hum
24	50.5	56.1	1216	2	JW0105	synaptojanin 2 alp
25	50	55.6	192	2	S76867	hypothetical prote
26	50	55.6	383	2	T06753	zinc finger protei
27	50	55.6	415	1	A34170	acrosin (EC 3.4.21
28	50	55.6	421	2	S29599	acrosin (EC 3.4.21
29	50	55.6	424	2	A54964	spliceosome-associ
30	50	55.6	449	2	S16748	proline-rich prote
31	50	55.6	547	2	C96828	unknown protein F1
32	50	55.6	1460	1	EDBEIF	immediate-early pr
33	50	55.6	3036	2	T18995	hypothetical prote
34	49.5	55.0	589	2	T29299	hypothetical prote
35	49	54.4	118	2	T19345	hypothetical prote
36	49	54.4	134	2	JC5572	proline-rich prote
37	49	54.4	161	2	F72593	hypothetical prote
38	49	54.4	210	2	T33700	hypothetical prote
39	49	54.4	218	2	T22261	hypothetical prote
40	49	54.4	296	2	A27319	gliadin - wheat
41	49	54.4	296	2	S07361	alpha/beta-gliadin
42	49	54.4	352	2	F84799	hypothetical prote
43	49	54.4	369	2	S20500	hydroxyproline-ric
44	49	54.4	380	2	T32944	hypothetical prote
45	49	54.4	413	2	H87604	hypothetical prote

ALIGNMENTS

RESULT 1
S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N;Alternate names: myeloid antibacterial protein PR-39
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68232; JN0899; I47138; S19563
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: propheni
A;Reference number: S68232; MUID:96105365; PMID:7498526
A;Accession: S68232
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-172 <ZHA>
A;Cross-references: EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g1165151
A;Experimental source: leukocytes
R;Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the i
A;Reference number: JN0899; MUID:94071853; PMID:8250863
A;Accession: JN0899
A;Molecule type: mRNA
A;Residues: 1-20,'A',22-172 <STO>
A;Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101
A;Experimental source: bone marrow cells
R;Gudmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.; Boma
Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A;Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fami
A;Reference number: I47138; MUID:95350216; PMID:7624374
A;Accession: I47138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-28,'T',30-89,'QR',92-116,'NDP',120-172 <GUD>
A;Cross-references: EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PID:g1051298
R;Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall,
Eur. J. Biochem. 202, 849-854, 1991
A;Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of th
A;Reference number: S19563; MUID:92111534; PMID:1765098
A;Accession: S19563
A;Molecule type: protein
A;Residues: 131-169 <AGE>
A;Experimental source: intestine
C;Genetics:
A;Gene: PR39
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>

F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl

Query Match 100.0%; Score 90; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RRRPRPPYLPRPRPP 15
          |||||||||||||||
Db    131 RRRPRPPYLPRPRPP 145
```

RESULT 2
A36589
bactenecin 7 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-May-1997
C;Accession: A36589
R;Frank, R.W.; Gennaro, R.; Schneider, K.; Przybylski, M.; Romeo, D.
J. Biol. Chem. 265, 18871-18874, 1990
A;Title: Amino acid sequences of two proline-rich bactenecins. Antimicrobial peptides of
A;Reference number: A36589; MUID:91035404; PMID:2229048
A;Accession: A36589
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-59 <FRA>
C;Superfamily: cathelin; cystatin homology

Query Match 73.3%; Score 66; DB 2; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.086;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 RRRPRPPYLPRPRP 14
          | ||||| ||||||
Db      2 RIRPRPPRLPRPRP 15
```

RESULT 3
A41051
spore coat protein precursor - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 03-Apr-1992 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2002
C;Accession: S04835; A41051; F69606
R;Aronson, A.I.; Song, H.Y.; Bourne, N.
Mol. Microbiol. 3, 437-444, 1989
A;Title: Gene structure and precursor processing of a novel Bacillus subtilis spore coat
A;Reference number: S04835; MUID:89313296; PMID:2546006
A;Accession: S04835
A;Molecule type: DNA
A;Residues: 'MNVHTPNLSIRNMVKGIKKAREVFLL',2-82 <AR2>
A;Cross-references: EMBL:X13740; NID:g39864; PIDN:CAA32004.1; PID:g39865
A;Experimental source: strain JH642
A;Note: part of this sequence, including the amino end of the mature protein, was confir
R;Bourne, N.; FitzJames, P.C.; Aronson, A.I.
J. Bacteriol. 173, 6618-6625, 1991
A;Title: Structural and germination defects of Bacillus subtilis spores with altered cor
A;Reference number: A41051; MUID:92011439; PMID:1917883
A;Accession: A41051
A;Molecule type: protein
A;Residues: 'XX',3-11 <BOU>
A;Experimental source: strain JH642
A;Note: the material sequenced was the larger of two isolated precursor forms; the amino
A;Note: both the location of the transcription start site and peptide sequencing of the
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69606
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'MNVHTPNLSIRNMVKGIKKAREVFLL',2-82 <KUN>
A;Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13066.1; PID:g2633563
A;Experimental source: strain 168
C;Comment: This structural protein is expressed during stage V of sporulation.
C;Genetics:
A;Gene: cotT
A;Start codon: TTG
C;Keywords: sporulation
F;1-19/Domain: propeptide #status experimental <PRO>
F;20-82/Product: spore coat protein #status experimental <MAT>

Query Match 66.1%; Score 59.5; DB 2; Length 82;
Best Local Similarity 84.6%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy      4 PRPP-YLPRPRPP 15
          |||| | ||||||
Db     49 PRPPYYYPRPRPP 61
```

RESULT 4
S68230
antimicrobial peptide precursor - sheep
N;Alternate names: Bac7.5 peptide homolog
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S68230
R;Bagella, L.; Scocchi, M.; Zanetti, M.
FEBS Lett. 376, 225-228, 1995
A;Title: cDNA sequences of three sheep myeloid cathelicidins.
A;Reference number: S68228; MUID:96105386; PMID:7498547
A;Accession: S68230
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-190 <BAG>
A;Cross-references: EMBL:L46852; NID:g1161244; PIDN:AAA85468.1; PID:g1161245
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;29-130/Domain: propeptide #status predicted <PRO>
F;130-190/Product: antimicrobial peptide #status predicted <MAT>

Query Match 64.4%; Score 58; DB 2; Length 190;
Best Local Similarity 78.6%; Pred. No. 2.4;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 RRRPRPPYLPRPRP 14
          | ||| | ||||||
Db    132 RLRPRRPRLPRPRP 145
```

RESULT 5
S35330
apidaecin 14 precursor - honeybee
N;Contains: apidaecin II
C;Species: Apis mellifera (honeybee)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S35330; S06676
R;Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.
EMBO J. 12, 1569-1578, 1993
A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplificati
A;Reference number: S35330; MUID:93223697; PMID:8467807
A;Accession: S35330
A;Molecule type: mRNA
A;Residues: 1-168 <CAS>

A;Cross-references: EMBL:X72575; NID:g297062; PIDN:CAA51167.1; PID:g297063
R;Casteels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.
EMBO J. 8, 2387-2391, 1989
A;Title: Apidaecins: antibacterial peptides from honeybees.
A;Reference number: S05383; MUID:90005446; PMID:2676519
A;Accession: S06676
A;Molecule type: protein
A;Residues: 43-60 <CA2>
C;Superfamily: procyclic acidic repetitive protein
F;43-60/Product: apidaecin II #status experimental <MAT>

Query Match 62.8%; Score 56.5; DB 2; Length 168;
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 11; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

Qy 1 RRRP-------RPPYLPRPRPP 15
|| | || |:|:||||
Db 117 RREPEAEPGNNRPVYIPQPRPP 138

RESULT 6
S14981
extensin class I (clone w1-8 L) - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
C;Accession: S14981
R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response t
A;Reference number: S14970; MUID:91329690; PMID:1714316
A;Accession: S14981
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-199 <SHO>
A;Cross-references: EMBL:X55692
A;Experimental source: cv. UC82B
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 62.8%; Score 56.5; DB 2; Length 199;
Best Local Similarity 73.3%; Pred. No. 3.7;
Matches 11; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 4 PRPP---YLPRPRPP 15
|||| ||| ||||
Db 77 PRPPPPEYLPPPRPP 91

RESULT 7
A88942
protein R13D11.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: A88942
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A88942
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-437 <STO>
A;Cross-references: GB:chr_V; PIDN:AAB69949.1; PID:g2384928; GSPDB:GN00023; CESP:R13D11.
C;Genetics:
A;Gene: R13D11.3
A;Map position: 5

Query Match 61.1%; Score 55; DB 2; Length 437;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PRPPYLPRPRPP 15
||||: | ||||
Db 23 PRPPHPPIPRPP 34

RESULT 8
JQ1663
hybrid proline-rich protein - maize
C;Species: Zea mays (maize)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C;Accession: JQ1663
R;Jose-Estanyol, M.; Ruiz-Avila, L.; Puigdomenech, P.
Plant Cell 4, 413-423, 1992
A;Title: A maize embryo-specific gene encodes a proline-rich and hydrophobic protein.
A;Reference number: JQ1663; MUID:92361259; PMID:1498600
A;Accession: JQ1663
A;Molecule type: DNA
A;Residues: 1-301 <JOS>
A;Cross-references: EMBL:X60432; NID:g433706; PIDN:CAA42959.1; PID:g433707
A;Experimental source: strain W64A
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 60.6%; Score 54.5; DB 2; Length 301;
Best Local Similarity 71.4%; Pred. No. 9.7;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 3 RPRPPYL-PRPRPP 15
|| |||: | ||||
Db 149 RPSPPYVPPTPRPP 162

RESULT 9
T13478
hypothetical protein 34F3.10 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13478
R;Valenti, P.; Salles, C.; Campbell, L.; Glover, D.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17685
A;Accession: T13478
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 <PHI>
A;Cross-references: EMBL:AL031583; NID:e1321005; PID:e1321018; PIDN:CAB41346.1
C;Genetics:
A;Cross-references: FlyBase:FBgn0025623
A;Introns: 17/2; 50/3; 333/2
A;Note: EG:34F3.10

Query Match 60.0%; Score 54; DB 2; Length 359;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 RRPRPPYLPRPRPP 15
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Db 167 RRPPPPPLPPPPPP 180

RESULT 10
T32652
hypothetical protein F39C12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T32652
R;Chissoe, S.; Sansone, J.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F39C12.
A;Reference number: Z21206
A;Accession: T32652
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

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A;Residues: 1-427 <CHI>
A;Cross-references: EMBL:AF039043; PIDN:AAB94196.1; GSPDB:GN00028; CESP:F39C12.3
A;Experimental source: strain Bristol N2; clone F39C12
C;Genetics:
A;Gene: CESP:F39C12.3
A;Map position: X
A;Introns: 42/3; 104/3; 133/3; 164/3; 213/3; 276/3; 336/3

  Query Match             60.0%;  Score 54;  DB 2;  Length 427;
  Best Local Similarity   69.2%;  Pred. No. 16;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 RPRPPYLPRPRPP 15
          ||||| :| | ||
Db    338 RPRPPDIPPPLPP 350


RESULT 11
S06675
apidaecin Ib precursor - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Dec-1998
C;Accession: S06675
R;Casteels, P.; Ampe, C.; Jacobs, F.; Vaeck, M.; Tempst, P.
EMBO J. 8, 2387-2391, 1989
A;Title: Apidaecins: antibacterial peptides from honeybees.
A;Reference number: S05383; MUID:90005446; PMID:2676519
A;Accession: S06675
A;Molecule type: protein
A;Residues: 1-26 <CAS>
F;1-8/Domain: propeptide #status experimental <PRO>
F;9-26/Product: apidaecin Ib #status experimental <MAT>

  Query Match             58.9%;  Score 53;  DB 2;  Length 26;
  Best Local Similarity   72.7%;  Pred. No. 1.3;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 RPPYLPRPRPP 15
          || |:|:|||| 
Db     12 RPVYIPQPRPP 22


RESULT 12
S35331
apidaecin 22 precursor - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: S35331
R;Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.
EMBO J. 12, 1569-1578, 1993
A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplificat
A;Reference number: S35330; MUID:93223697; PMID:8467807
A;Accession: S35331
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-144 <CAS>
A;Cross-references: EMBL:X72576; NID:g297064; PIDN:CAA51168.1; PID:g297065
C;Superfamily: procyclic acidic repetitive protein

  Query Match             58.9%;  Score 53;  DB 2;  Length 144;
  Best Local Similarity   72.7%;  Pred. No. 7.1;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 RPPYLPRPRPP 15
          || |:|:|||| 
Db    102 RPVYIPQPRPP 112


RESULT 13
T29373
hypothetical protein ZC404.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T29373
R;Bentley, D.; Le, T.T.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid ZC404.
A;Reference number: Z20614
A;Accession: T29373
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-184 <BEN>
A;Cross-references: EMBL:U55363; PIDN:AAA97967.1; GSPDB:GN00023; CESP:ZC404.1
A;Experimental source: strain Bristol N2; clone ZC404
C;Genetics:
A;Gene: CESP:ZC404.1
A;Map position: 5
A;Introns: 15/2; 50/2; 75/2; 138/2
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC404.1

  Query Match             58.9%;  Score 53;  DB 2;  Length 184;
  Best Local Similarity   90.0%;  Pred. No. 9;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 RPRPPYLPRP 12
          ||| ||||||
Db     26 RPRKPYLPRP 35


RESULT 14
S35332
apidaecin 73 precursor - honeybee (fragment)
N;Contains: apidaecin Ia
C;Species: Apis mellifera (honeybee)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Nov-2000
C;Accession: S35332; S05383
R;Casteels-Josson, K.; Capaci, T.; Casteels, P.; Tempst, P.
EMBO J. 12, 1569-1578, 1993
A;Title: Apidaecin multipeptide precursor structure: a putative mechanism for amplificati
A;Reference number: S35330; MUID:93223697; PMID:8467807
A;Accession: S35332
A;Molecule type: mRNA
A;Residues: 1-283 <CAS>
A;Cross-references: EMBL:X72577; NID:g297066; PIDN:CAA51169.1; PID:g4539289
A;Accession: S05383
A;Molecule type: protein
A;Residues: 258-283 <CA3>
C;Superfamily: proline-rich protein
F;266-283/Product: apidaecin Ia #status experimental <MAT>

  Query Match             58.9%;  Score 53;  DB 2;  Length 283;
  Best Local Similarity   72.7%;  Pred. No. 14;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 RPPYLPRPRPP 15
          || |:|:|||| 
Db    241 RPVYIPQPRPP 251


RESULT 15
E71415
probable coll wall protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C;Accession: E71415
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirke
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giele
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ansc
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thali
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: E71415
```

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-428 <BEV>
A;Cross-references: GB:Z97338; NID:g2244870; PID:e327461; PID:g2244874
C;Genetics:
A;Map position: 4COP9-4G3845

Query Match 58.9%; Score 53; DB 2; Length 428;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy       3 RPRPPYLPRPRPP 15
           :| |||:| | ||
Db      67 KPPPPYIPCPPPP 79
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Search completed: May 13, 2003, 10:41:48
Job time : 18 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 13, 2003, 10:34:02 ; Search time 11 Seconds
(without alignments)
56.559 Million cell updates/sec

Title: US-09-426-011D-3
Perfect score: 90
Sequence: 1 RRRPRPPYLPRPRPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	172	1	PR39_PIG	P80054 sus scrofa
2	66	73.3	190	1	BCT7_BOVIN	P19661 bos taurus
3	59.5	66.1	107	1	COTT_BACSU	P11863 bacillus su
4	58	64.4	190	1	BCT7_SHEEP	P50415 ovis aries
5	56.5	62.8	168	1	AP14_APIME	Q06601 apis mellif
6	55.5	61.7	151	1	RNB_HSV2H	P89479 herpes simp
7	53	58.9	144	1	AP22_APIME	P35581 apis mellif
8	53	58.9	283	1	AP73_APIME	Q06602 apis mellif
9	53	58.9	381	1	PRLP_BOVIN	Q9gkn8 bos taurus
10	52	57.8	261	1	RL1_HSV2H	P28283 herpes simp
11	52	57.8	354	1	ATH1_HUMAN	Q92858 homo sapien
12	52	57.8	467	1	AFC1_ARATH	P51566 arabidopsis
13	52	57.8	841	1	RELA_STRAT	O85709 streptomyce
14	51.5	57.2	1187	1	PTNE_HUMAN	Q15678 homo sapien
15	51.5	57.2	1189	1	PTNE_MOUSE	Q62130 mus musculu
16	51	56.7	15	1	MK1_PALPR	P80408 palomena pr
17	51	56.7	180	1	XG_HUMAN	P55808 homo sapien
18	50.5	56.1	393	1	CIW4_HUMAN	Q9nyg8 homo sapien
19	50	55.6	17	1	APID_BOMPA	P81464 bombus pasc
20	50	55.6	415	1	ACRO_PIG	P08001 sus scrofa
21	50	55.6	424	1	S3B4_HUMAN	Q15427 homo sapien
22	50	55.6	449	1	APG_BRANA	P40603 brassica na
23	50	55.6	678	1	ABPP_RIPCL	Q27905 riptortus c
24	49	54.4	134	1	PRL5_HUMAN	Q99954 homo sapien
25	49	54.4	296	1	GDA6_WHEAT	P04726 triticum ae
26	49	54.4	352	1	RRS1_ARATH	Q9sh88 arabidopsis
27	49	54.4	2911	1	FBN2_HUMAN	P35556 homo sapien
28	48.5	53.9	2142	1	BAT2_HUMAN	P48634 homo sapien
29	48	53.3	280	1	TNF6_CERTO	Q9bdn1 cercocebus
30	48	53.3	280	1	TNF6_MACMU	Q9myl6 macaca mula
31	48	53.3	281	1	TNF6_HUMAN	P48023 homo sapien
32	48	53.3	282	1	TNF6_PIG	Q9bea8 sus scrofa
33	48	53.3	402	1	VGLD_PRVRI	P07645 pseudorabie
34	48	53.3	520	1	C84A_ARATH	Q42600 arabidopsis
35	48	53.3	759	1	TOP3_CAEEL	O61660 caenorhabdi
36	47.5	52.8	283	1	EXTN_SORBI	P24152 sorghum bic
37	47.5	52.8	372	1	DBPA_HUMAN	P16989 homo sapien
38	47.5	52.8	1443	1	SYJ2_HUMAN	O15056 homo sapien
39	47	52.2	176	1	BCT5_BOVIN	P19660 bos taurus
40	47	52.2	261	1	PRP2_MOUSE	P05142 mus musculu
41	47	52.2	296	1	PRP3_MOUSE	P05143 mus musculu
42	47	52.2	507	1	MEFA_HUMAN	Q02078 homo sapien
43	47	52.2	753	1	SX30_HUMAN	O94993 homo sapien
44	47	52.2	846	1	IRS1_HCMVA	P09715 human cytom
45	47	52.2	1040	1	BOI2_YEAST	P39969 saccharomyc

ALIGNMENTS

RESULT 1
PR39_PIG
ID PR39_PIG STANDARD; PRT; 172 AA.
AC P80054; Q9TR84;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antibacterial protein PR-39 precursor.
GN PR39.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95350216; PubMed=7624374;
RA Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M.,
RA Andersson L., Boman H.G.;
RT "Structure of the gene for porcine peptide antibiotic PR-39, a
RT cathelin gene family member: comparative mapping of the locus for the
RT human peptide antibiotic FALL-39.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=94071853; PubMed=8250863;
RA Storici P., Zanetti M.;
RT "A cDNA derived from pig bone marrow cells predicts a sequence
RT identical to the intestinal antibacterial peptide PR-39.";
RL Biochem. Biophys. Res. Commun. 196:1058-1065(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96105365; PubMed=7498526;
RA Zhao C., Ganz T., Lehrer R.I.;
RT "Structures of genes for two cathelin-associated antimicrobial
RT peptides: prophenin-2 and PR-39.";
RL FEBS Lett. 376:130-134(1995).
RN [4]
RP SEQUENCE OF 131-169.
RC TISSUE=Intestine;
RX MEDLINE=92111534; PubMed=1765098;
RA Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
RA Mutt V., Joernvall H.;
RT "Amino acid sequence of PR-39. Isolation from pig intestine of a new
RT member of the family of proline-arginine-rich antibacterial
RT peptides.";
RL Eur. J. Biochem. 202:849-854(1991).
RN [5]
RP SEQUENCE OF 131-164, AND FUNCTION.
RC TISSUE=Neutrophils;
RX MEDLINE=95088504; PubMed=7996056;
RA Shi J., Ross C.R., Chengappa M.M., Blecha F.;
RT "Identification of a proline-arginine-rich antibacterial peptide from
RT neutrophils that is analogous to PR-39, an antibacterial peptide from
RT the small intestine.";

```
RL   J. Leukoc. Biol. 56:807-811(1994).
CC   -!- FUNCTION: EXERTS A POTENT ANTIMICROBIAL ACTIVITY AGAINST BOTH
CC       E.COLI AND B.MEGATERIUM.
CC   -!- TISSUE SPECIFICITY: SMALL INTESTINE AND BONE MARROW.
CC   -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X87236; CAA60682.1; -.
DR   EMBL; L23825; AAA31109.1; -.
DR   EMBL; X89201; CAA61487.1; -.
DR   PIR; S19563; S19563.
DR   InterPro; IPR001894; Cathelicidin.
DR   Pfam; PF00666; Cathelicidins; 1.
DR   ProDom; PD001838; Cathelicidin; 1.
DR   PROSITE; PS00946; CATHELICIDINS_1; 1.
DR   PROSITE; PS00947; CATHELICIDINS_2; 1.
KW   Antibiotic; Amidation; Signal.
FT   SIGNAL       1     29       POTENTIAL.
FT   PROPEP      30    130
FT   CHAIN      131    169       ANTIBACTERIAL PROTEIN PR-39.
FT   MOD_RES     30     30       PYRROLIDONE CARBOXYLIC ACID (BY
FT                               SIMILARITY).
FT   DISULFID    85     96       BY SIMILARITY.
FT   DISULFID   107    124       BY SIMILARITY.
FT   MOD_RES    169    169       AMIDATION (G-170 PROVIDE AMIDE GROUP).
FT   CONFLICT    21     21       G -> A (IN REF. 2).
FT   CONFLICT    29     29       A -> T (IN REF. 1).
FT   CONFLICT    90     91       RQ -> QR (IN REF. 1).
FT   CONFLICT   117    119       IHS -> NDP (IN REF. 1).
FT   CONFLICT   157    157       P -> I (IN REF. 5).
SQ   SEQUENCE   172 AA;  19476 MW;  994B792798C0E133 CRC64;

  Query Match           100.0%;  Score 90;  DB 1;  Length 172;
  Best Local Similarity  100.0%;  Pred. No. 0.00022;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           |||||||||||||||
Db     131 RRRPRPPYLPRPRPP 145


RESULT 2
BCT7_BOVIN
ID   BCT7_BOVIN     STANDARD;      PRT;   190 AA.
AC   P19661;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Bactenecin 7 precursor (BAC7) (PR-59).
GN   BAC7.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=95010707; PubMed=7925973;
RA   Scocchi M., Romeo D., Zanetti M.;
RT   "Molecular cloning of Bac7, a proline- and arginine-rich
RT   antimicrobial peptide from bovine neutrophils.";
RL   FEBS Lett. 352:197-200(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Scocchi M., Wang S., Zanetti M.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 131-189.
RC   TISSUE=Neutrophils;
RX   MEDLINE=91035404; PubMed=2229048;
RA   Frank R.W., Gennaro R., Schneider K., Przybylski M., Romeo D.;
RT   "Amino acid sequences of two proline-rich bactenecins. Antimicrobial
RT   peptides of bovine neutrophils.";
RL   J. Biol. Chem. 265:18871-18874(1990).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=96300243; PubMed=8706679;
RA   Storici P., Tossi A., Lenarcic B., Romeo D.;
RT   "Purification and structural characterization of bovine
RT   cathelicidins, precursors of antimicrobial peptides.";
RL   Eur. J. Biochem. 238:769-776(1996).
CC   -!- FUNCTION: EXERTS, IN VITRO, A POTENT ANTIMICROBIAL ACTIVITY.
CC       PROBABLY DUE TO AN IMPAIRMENT OF THE FUNCTION OF THE RESPIRATORY
CC       CHAIN AND OF ENERGY-DEPENDENT ACTIVITIES IN THE INNER MEMBRANE
CC       OF SUSCEPTIBLE MICROORGANISMS.
CC   -!- TISSUE SPECIFICITY: LARGE GRANULES OF NEUTROPHILS.
CC   -!- PTM: ELASTASE IS RESPONSIBLE FOR ITS MATURATION.
CC   -!- MASS SPECTROMETRY: MW=18395; MW_ERR=1; METHOD=Electrospray;
CC       RANGE=30-190.
CC   -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L42977; AAA87359.1; -.
DR   EMBL; Y09471; CAA70616.1; -.
DR   PIR; A36589; A36589.
DR   InterPro; IPR001894; Cathelicidin.
DR   Pfam; PF00666; Cathelicidins; 1.
DR   ProDom; PD001838; Cathelicidin; 1.
DR   PROSITE; PS00946; CATHELICIDINS_1; 1.
DR   PROSITE; PS00947; CATHELICIDINS_2; 1.
KW   Antibiotic; Repeat; Signal.
FT   SIGNAL       1     29       POTENTIAL.
FT   PROPEP      30    130
FT   CHAIN      131    190       BACTENECIN 7.
FT   PROPEP     189    190       REMOVED PARTIALLY.
FT   MOD_RES     30     30       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID    85     96
FT   DISULFID   107    124
SQ   SEQUENCE   190 AA;  21567 MW;  8CD07D7AA30A731C CRC64;

  Query Match           73.3%;  Score 66;  DB 1;  Length 190;
  Best Local Similarity  85.7%;  Pred. No. 0.15;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRP 14
           | ||||| ||||||
Db     132 RIRPRPPRLPRPRP 145


RESULT 3
COTT_BACSU
ID   COTT_BACSU     STANDARD;      PRT;   107 AA.
AC   P11863;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Spore coat protein T precursor.
GN   COTT.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
```

```
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168 / JH642;
RX   MEDLINE=89313296; PubMed=2546006;
RA   Aronson A.I., Song H.Y., Bourne N.;
RT   "Gene structure and precursor processing of a novel Bacillus subtilis
RT   spore coat protein.";
RL   Mol. Microbiol. 3:437-444(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA   Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA   Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA   Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA   Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA   Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA   Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA   Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA   Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA   Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA   Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA   Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA   Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA   Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA   Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA   Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA   Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA   Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
CC   -!- FUNCTION: POSSIBLY PROTECTION OF SPORE AND PROBABLY PLAYS
CC       SOME ROLE IN GERMINATION.
CC   -!- SUBCELLULAR LOCATION: OUTER SURFACE OF ENDOSPORE.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X13740; CAA32004.1; -.
DR   EMBL; Z99110; CAB13066.1; -.
DR   PIR; S04835; S04835.
DR   SubtiList; BG10495; cotT.
KW   Sporulation; Signal; Complete proteome.
FT   SIGNAL       1     44
FT   CHAIN       45    107       SPORE COAT PROTEIN T.
SQ   SEQUENCE   107 AA;  12992 MW;  AD1F66F0C4CE29A3 CRC64;

  Query Match             66.1%;  Score 59.5;  DB 1;  Length 107;
  Best Local Similarity   84.6%;  Pred. No. 0.47;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       4 PRPP-YLPRPRPP 15
           |||| | ||||||
Db      74 PRPPYYYPRPRPP 86
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RESULT 4
BCT7_SHEEP
ID   BCT7_SHEEP     STANDARD;      PRT;   190 AA.
AC   P50415;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Bactenecin 7 precursor (BAC7).
GN   BAC7.5.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=96105386; PubMed=7498547;
RA   Bagella L., Scocchi M., Zanetti M.;
RT   "cDNA sequences of three sheep myeloid cathelicidins.";
RL   FEBS Lett. 376:225-228(1995).
CC   -!- FUNCTION: EXERTS, IN VITRO, A POTENT ANTIMICROBIAL ACTIVITY.
CC       PROBABLY DUE TO AN IMPAIRMENT OF THE FUNCTION OF THE RESPIRATORY
CC       CHAIN AND OF ENERGY-DEPENDENT ACTIVITIES IN THE INNER MEMBRANE
CC       OF SUSCEPTIBLE MICROORGANISMS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L46852; AAA85468.1; -.
DR   InterPro; IPR001894; Cathelicidin.
DR   Pfam; PF00666; Cathelicidins; 1.
DR   ProDom; PD001838; Cathelicidin; 1.
DR   PROSITE; PS00946; CATHELICIDINS_1; 1.
DR   PROSITE; PS00947; CATHELICIDINS_2; 1.
KW   Antibiotic; Repeat; Signal.
FT   SIGNAL       1     29       POTENTIAL.
FT   PROPEP      30    130       BY SIMILARITY.
FT   CHAIN      131    190       BACTENECIN 7.
FT   MOD_RES     30     30       PYRROLIDONE CARBOXYLIC ACID
FT                               (BY SIMILARITY).
FT   DISULFID    85     96       BY SIMILARITY.
FT   DISULFID   107    124       BY SIMILARITY.
SQ   SEQUENCE   190 AA;  21829 MW;  E4AAFB1600E98371 CRC64;

  Query Match             64.4%;  Score 58;  DB 1;  Length 190;
  Best Local Similarity   78.6%;  Pred. No. 1.2;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRP 14
           | ||| | ||||||
Db     132 RLRPRRPRLPRPRP 145


RESULT 5
AP14_APIME
ID   AP14_APIME     STANDARD;      PRT;   168 AA.
AC   Q06601; P11525; P11526; P11527;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   Apidaecin precursor, type 14.
GN   APID14.
OS   Apis mellifera (Honeybee).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
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OC   Aculeata; Apoidea; Apidae; Apis.
OX   NCBI_TaxID=7460;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93223697; PubMed=8467807;
RA   Casteels-Josson K., Capaci T., Casteels P., Tempst P.;
RT   "Apidaecin multipeptide precursor structure: a putative mechanism for
RT   amplification of the insect antibacterial response.";
RL   EMBO J. 12:1569-1578(1993).
RN   [2]
RP   SEQUENCE OF APIDAECINS IA/IB/II.
RC   TISSUE=Hemolymph;
RX   MEDLINE=90005446; PubMed=2676519;
RA   Casteels P., Ampe C., Jacobs F., Vaeck M., Tempst P.;
RT   "Apidaecins: antibacterial peptides from honeybees.";
RL   EMBO J. 8:2387-2391(1989).
CC   -!- FUNCTION: APIDAECINS HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
CC       AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
CC       PROPAGATION.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X72575; CAA51167.1; -.
DR   PIR; S05383; S05383.
DR   PIR; S06675; S06675.
DR   PIR; S06676; S06676.
DR   PIR; S35330; S35330.
DR   InterPro; IPR004828; Apidaecin.
DR   Pfam; PF00807; Apidaecin; 5.
KW   Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW   Cleavage on pair of basic residues; Repeat.
FT   SIGNAL       1     19       POTENTIAL.
FT   PROPEP      35     42
FT   PEPTIDE     43     60       APIDAECIN II.
FT   PROPEP      63     70
FT   PEPTIDE     71     88       APIDAECIN II.
FT   PROPEP      91     98
FT   PEPTIDE     99    116       APIDAECIN IB.
FT   PROPEP     119    124
FT   PEPTIDE    125    142       APIDAECIN IB.
FT   PROPEP     145    150
FT   PEPTIDE    151    168       APIDAECIN IA.
SQ   SEQUENCE   168 AA;  19380 MW;  594B931254C04A37 CRC64;

  Query Match             62.8%;  Score 56.5;  DB 1;  Length 168;
  Best Local Similarity   50.0%;  Pred. No. 1.6;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    7;  Gaps    1;

Qy       1 RRRP-------RPPYLPRPRPP 15
           || |       || |:|:|||| 
Db     117 RREPEAEPGNNRPVYIPQPRPP 138


RESULT 6
RNB_HSV2H
ID   RNB_HSV2H      STANDARD;      PRT;   151 AA.
AC   P89479;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Potential RNA-binding protein.
GN   US11.
OS   Herpes simplex virus (type 2 / strain HG52).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10315;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dolan A.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: BINDS DNA AND RNA (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z86099; CAB06719.1; -.
KW   DNA-binding; RNA-binding; Repeat; Nuclear protein.
FT   DOMAIN       90    146       11 X 6 AA TANDEM REPEATS.
FT   REPEAT       90     95       1.
FT   REPEAT       96    101       2.
FT   REPEAT      102    104       3.
FT   REPEAT      105    110       4.
FT   REPEAT      111    116       5.
FT   REPEAT      117    122       6.
FT   REPEAT      123    128       7.
FT   REPEAT      129    130       8.
FT   REPEAT      131    134       9.
FT   REPEAT      135    140       10.
FT   REPEAT      141    146       11.
SQ   SEQUENCE   151 AA;  16297 MW;  FAB751F23C3DB6AE CRC64;

  Query Match             61.7%;  Score 55.5;  DB 1;  Length 151;
  Best Local Similarity   73.3%;  Pred. No. 1.9;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       2 RRPRPPYLPR-PRPP 15
           | |||| :|| ||||
Db     127 RPPRPPRVPREPRPP 141


RESULT 7
AP22_APIME
ID   AP22_APIME     STANDARD;      PRT;   144 AA.
AC   P35581; P11525; P11526;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   Apidaecin precursor, type 22.
OS   Apis mellifera (Honeybee).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC   Aculeata; Apoidea; Apidae; Apis.
OX   NCBI_TaxID=7460;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93223697; PubMed=8467807;
RA   Casteels-Josson K., Capaci T., Casteels P., Tempst P.;
RT   "Apidaecin multipeptide precursor structure: a putative mechanism for
RT   amplification of the insect antibacterial response.";
RL   EMBO J. 12:1569-1578(1993).
RN   [2]
RP   SEQUENCE (APIDAECINS IA/IB).
RC   TISSUE=Hemolymph;
RX   MEDLINE=90005446; PubMed=2676519;
RA   Casteels P., Ampe C., Jacobs F., Vaeck M., Tempst P.;
RT   "Apidaecins: antibacterial peptides from honeybees.";
RL   EMBO J. 8:2387-2391(1989).
CC   -!- FUNCTION: APIDAECINS HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
CC       AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
CC       PROPAGATION.
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CC   ----------------------------------------------------------------------
DR   EMBL; X72576; CAA51168.1; -.
DR   PIR; S05383; S05383.
DR   PIR; S06675; S06675.
DR   PIR; S35331; S35331.
DR   InterPro; IPR004828; Apidaecin.
DR   Pfam; PF00807; Apidaecin; 4.
KW   Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW   Cleavage on pair of basic residues; Repeat.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       35     42
FT   PEPTIDE      43     60       APIDAECIN IB.
FT   PROPEP       63     70
FT   PEPTIDE      71     88       APIDAECIN IB.
FT   PROPEP       91     98
FT   PEPTIDE      99    116       APIDAECIN IB.
FT   PROPEP.     119    126
FT   PEPTIDE     127    144       APIDAECIN IA.
SQ   SEQUENCE   144 AA;  16539 MW;  6FA1AD74CB77108D CRC64;

  Query Match             58.9%;  Score 53;  DB 1;  Length 144;
  Best Local Similarity   72.7%;  Pred. No. 3.6;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 RPPYLPRPRPP 15
           || |:|:|||| 
Db     102 RPVYIPQPRPP 112


RESULT 8
AP73_APIME
ID   AP73_APIME     STANDARD;      PRT;   283 AA.
AC   Q06602; P11525; P11526;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   Apidaecin precursor, type 73 (Fragment).
GN   APID73.
OS   Apis mellifera (Honeybee).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC   Aculeata; Apoidea; Apidae; Apis.
OX   NCBI_TaxID=7460;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93223697; PubMed=8467807;
RA   Casteels-Josson K., Capaci T., Casteels P., Tempst P.;
RT   "Apidaecin multipeptide precursor structure: a putative mechanism for
RT   amplification of the insect antibacterial response.";
RL   EMBO J. 12:1569-1578(1993).
RN   [2]
RP   SEQUENCE OF APIDAECINS IA/IB.
RC   TISSUE=Hemolymph;
RX   MEDLINE=90005446; PubMed=2676519;
RA   Casteels P., Ampe C., Jacobs F., Vaeck M., Tempst P.;
RT   "Apidaecins: antibacterial peptides from honeybees.";
RL   EMBO J. 8:2387-2391(1989).
CC   -!- FUNCTION: APIDAECINS HAVE BACTERICIDAL ACTIVITY; PREDOMINANTLY
CC       AGAINST GRAM-NEGATIVE BACTERIA. THEY SEEM TO INTERFERE WITH CELL
CC       PROPAGATION.
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CC   ----------------------------------------------------------------------
DR   EMBL; X72577; CAA51169.1; -.
DR   PIR; S05383; S05383.
DR   PIR; S06675; S06675.
DR   PIR; S35332; S35332.
DR   InterPro; IPR004828; Apidaecin.
DR   Pfam; PF00807; Apidaecin; 9.
KW   Insect immunity; Antibiotic; Hemolymph; Signal; Multigene family;
KW   Cleavage on pair of basic residues; Repeat.
FT   NON_TER       1      1
FT   SIGNAL       <1     18       POTENTIAL.
FT   PROPEP       34     41
FT   PEPTIDE      42     59       APIDAECIN IB.
FT   PROPEP       62     69
FT   PEPTIDE      70     87       APIDAECIN IB.
FT   PROPEP       90     97
FT   PEPTIDE      98    115       APIDAECIN.
FT   PROPEP      118    125
FT   PEPTIDE     126    143       APIDAECIN IB.
FT   PROPEP      146    153
FT   PEPTIDE     154    171       APIDAECIN.
FT   PROPEP      174    182
FT   PEPTIDE     183    199       APIDAECIN IB.
FT   PROPEP      202    209
FT   PEPTIDE     210    227       APIDAECIN IB.
FT   PROPEP      230    237
FT   PEPTIDE     238    255       APIDAECIN IB.
FT   PROPEP      258    265
FT   PEPTIDE     266    283       APIDAECIN IA.
SQ   SEQUENCE   283 AA;  32695 MW;  4EA5FEDECD5E142B CRC64;

  Query Match             58.9%;  Score 53;  DB 1;  Length 283;
  Best Local Similarity   72.7%;  Pred. No. 6.9;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 RPPYLPRPRPP 15
           || |:|:|||| 
Db     241 RPVYIPQPRPP 251


RESULT 9
PRLP_BOVIN
ID   PRLP_BOVIN     STANDARD;      PRT;   381 AA.
AC   Q9GKN8;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Prolargin precursor (Proline-arginine-rich end leucine-rich repeat
DE   protein).
GN   PRELP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Articular cartilage;
RX   MEDLINE=20576219; PubMed=11007795;
RA   Bengtsson E., Aspberg A., Heinegaard D., Sommarin Y., Spillmann D.;
RT   "The amino-terminal part of PRELP binds to heparin and heparan
RT   sulfate.";
RL   J. Biol. Chem. 275:40695-40702(2000).
RN   [2]
RP   FUNCTION.
RX   PubMed=11847210;
RA   Bengtsson E., Morgelin M., Sasaki T., Timpl R., Heinegaard D.,
RA   Aspberg A.;
RT   "The leucine-rich repeat protein PRELP binds perlecan and collagens
RT   and may function as a basement membrane anchor.";
RL   J. Biol. Chem. 277:15061-15068(2002).
CC   -!- FUNCTION: May anchor basement membranes to the underlying
CC       connective tissue.
CC   -!- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan
```

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CC       perlecan and triple helical collagens type I and type II.
CC   -!- SUBCELLULAR LOCATION: Extracellular matrix.
CC   -!- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and
CC       heparan sulfate. Binds collagens type I and type II through its
CC       leucine-rich repeat domain.
CC   -!- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
CC       (SLRPS) FAMILY. CLASS II SUBFAMILY.
CC   -!- SIMILARITY: CONTAINS 12 LEUCINE-RICH REPEATS (LRR).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF163568; AAG23723.1; -.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003592; LRR_out.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00560; LRR; 10.
DR   Pfam; PF01462; LRRNT; 1.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00370; LRR; 7.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00369; LRR_TYP; 7.
KW   Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    381       PROLARGIN.
FT   DOMAIN       72     88       CYS-RICH.
FT   REPEAT       94    113       LRR-S 1.
FT   REPEAT      114    137       LRR-T 1.
FT   REPEAT      138    161       LRR-T 2.
FT   REPEAT      162    182       LRR-S 2.
FT   REPEAT      183    206       LRR-T 3.
FT   REPEAT      207    232       LRR-T 4.
FT   REPEAT      233    253       LRR-S 3.
FT   REPEAT      254    277       LRR-T 5.
FT   REPEAT      278    302       LRR-T 6.
FT   REPEAT      303    322       LRR-S 4.
FT   REPEAT      323    361       LRR-T 7.
FT   REPEAT      362    381       LRR-T 8.
FT   DOMAIN      196    201       POLY-LEU.
FT   DISULFID    331    372       BY SIMILARITY.
FT   CARBOHYD    123    123       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    288    288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    319    319       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    326    326       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   381 AA;  43682 MW;  23DA99C01BB772A0 CRC64;

  Query Match             58.9%;  Score 53;  DB 1;  Length 381;
  Best Local Similarity   76.9%;  Pred. No. 9.2;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 RRPRPPYLPRPRP 14
           |||||   |||||
Db      25 RRPRPRPRPRPRP 37


RESULT 10
RL1_HSV2H
ID   RL1_HSV2H      STANDARD;      PRT;   261 AA.
AC   P28283;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Neurovirulence factor (ICP34.5).
GN   RL1.
OS   Herpes simplex virus (type 2 / strain HG52).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Alphaherpesvirinae; Simplexvirus.
OX   NCBI_TaxID=10315;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92113549; PubMed=1662697;
RA   McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
RT   "Comparative sequence analysis of the long repeat regions and
RT   adjoining parts of the long unique regions in the genomes of herpes
RT   simplex viruses types 1 and 2.";
RL   J. Gen. Virol. 72:3057-3075(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Dolan A.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D10471; BAA23428.1; -.
DR   EMBL; Z86099; CAB06759.1; -.
DR   EMBL; Z86099; CAB06706.1; -.
DR   PIR; JQ1502; WMBEXE.
KW   Repeat.
FT   DOMAIN        3     12       2 X 5 AA TANDEM REPEATS OF R-R-R-G-P.
FT   REPEAT        3      7
FT   REPEAT        8     12
FT   DOMAIN       16     31       2 X 8 AA TANDEM REPEATS OF P-R-P-G-A-P-A-
FT                                V.
FT   REPEAT       16     23
FT   REPEAT       24     31
SQ   SEQUENCE   261 AA;  27908 MW;  4BBD13AF3D906D71 CRC64;

  Query Match             57.8%;  Score 52;  DB 1;  Length 261;
  Best Local Similarity   64.7%;  Pred. No. 8.3;
  Matches   11;  Conservative    1;  Mismatches    3;  Indels    2;  Gaps    1;

Qy       1 RRRPRP--PYLPRPRPP 15
           ||||||  | :|||  |
Db      13 RRRPRPGAPAVPRPGAP 29


RESULT 11
ATH1_HUMAN
ID   ATH1_HUMAN     STANDARD;      PRT;   354 AA.
AC   Q92858;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Atonal protein homolog 1 (Helix-loop-helix protein hATH-1).
GN   ATOH1 OR ATH1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97026280; PubMed=8872459;
RA   Ben-Arie N., McCall A.E., Berkman S., Eichele G., Bellen H.J.,
RA   Zoghbi H.Y.;
RT   "Evolutionary conservation of sequence and expression of the bHLH
RT   protein Atonal suggests a conserved role in neurogenesis.";
RL   Hum. Mol. Genet. 5:1207-1216(1996).
CC   -!- FUNCTION: ACTIVATES E BOX-DEPENDENT TRANSCRIPTION IN COLLABORATION
CC       WITH E47, BUT THE ACTIVITY IS COMPLETELY ANTAGONIZED BY THE
CC       NEGATIVE REGULATOR OF NEUROGENESIS HES-1. MAY PLAY A ROLE IN THE
CC       DIFFERENTIATION OF SUBSETS OF NEURAL CELLS BY ACTIVATING E BOX-
CC       DEPENDENT TRANSCRIPTION (BY SIMILARITY).
CC   -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
```

```
CC       BHLH PROTEIN.
CC   -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC   -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC       TRANSCRIPTION FACTORS. "ATONAL" SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U61148; AAB41305.1; -.
DR   TRANSFAC; T04544; -.
DR   Genew; HGNC:797; ATOH1.
DR   MIM; 601461; -.
DR   InterPro; IPR001092; HLH_basic.
DR   Pfam; PF00010; HLH; 1.
DR   SMART; SM00353; HLH; 1.
DR   PROSITE; PS00038; HLH_1; FALSE_NEG.
DR   PROSITE; PS50888; HLH_2; 1.
KW   Transcription regulation; Activator; DNA-binding; Nuclear protein.
FT   DOMAIN       29     38       POLY-PRO.
FT   DNA_BIND     160    171      BASIC DOMAIN.
FT   DOMAIN       172    212      HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT   DOMAIN       224    228      POLY-PRO.
SQ   SEQUENCE   354 AA;  38160 MW;  AB12F1E917A00A8D CRC64;

  Query Match             57.8%;  Score 52;  DB 1;  Length 354;
  Best Local Similarity   57.1%;  Pred. No. 11;
  Matches    8;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2 RRPRPPYLPRPRPP 15
           |:|:| :|.|:| ||
Db      21 RQPQPHHLPQPPPP 34


RESULT 12
AFC1_ARATH
ID   AFC1_ARATH     STANDARD;      PRT;   467 AA.
AC   P51566;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Protein kinase AFC1 (EC 2.7.1.-).
GN   AFC1.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Landsberg erecta;
RX   MEDLINE=95083650; PubMed=7991592;
RA   Bender J., Fink G.R.;
RT   "AFC1, a LAMMER kinase from Arabidopsis thaliana, activates STE12-
RT   dependent processes in yeast.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:12105-12109(1994).
CC   -!- FUNCTION: ACTIVATOR OF YEAST TRANSCRIPTION FACTOR, STE12.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       LAMMER SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U16176; AAA57117.1; -.
DR   HSSP; P24941; 1AQ1.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN       115    443      PROTEIN KINASE.
FT   NP_BIND      121    129      ATP (BY SIMILARITY).
FT   BINDING      144    144      ATP (BY SIMILARITY).
FT   ACT_SITE     240    240      BY SIMILARITY.
SQ   SEQUENCE   467 AA;  54216 MW;  54D739A82F490E12 CRC64;

  Query Match             57.8%;  Score 52;  DB 1;  Length 467;
  Best Local Similarity   52.4%;  Pred. No. 15;
  Matches   11;  Conservative    1;  Mismatches    3;  Indels    6;  Gaps    1;

Qy       1 RRRPR------PPYLPRPRPP 15
           |:|||      || || | ||
Db      35 RKRPRLTWDAAPPLLPPPPPP 55


RESULT 13
RELA_STRAT
ID   RELA_STRAT     STANDARD;      PRT;   841 AA.
AC   O85709;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   GTP pyrophosphokinase (EC 2.7.6.5) (ATP:GTP 3'-pyrophosphotransferase)
DE   (PPGPP synthetase I) ((P)PPGPP synthetase).
GN   RELA.
OS   Streptomyces antibioticus.
OC   Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1890;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IMRU 3720;
RX   MEDLINE=99296594; PubMed=10368159;
RA   Hoyt S., Jones G.H.;
RT   "relA is required for actinomycin production in Streptomyces
RT   antibioticus.";
RL   J. Bacteriol. 181:3824-3829(1999).
CC   -!- FUNCTION: In eubacteria PPGPP (guanosine 3'-diphosphate 5-'
CC       diphosphate) is a mediator of the stringent response that
CC       coordinates a variety of cellular activities in response to
CC       changes in nutritional abundance. This enzyme catalyzes the
CC       formation of PPPGPP which is then hydrolysed to form PPGPP (By
CC       similarity). Is required for actinomycin production.
CC   -!- CATALYTIC ACTIVITY: ATP + GTP = AMP + guanosine 3'-diphosphate 5'-
CC       triphosphate.
CC   -!- PATHWAY: FIRST STEP IN THE METABOLISM OF PPGPP.
CC   -!- SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF072829; AAC26021.1; -.
DR   InterPro; IPR002912; ACT.
DR   InterPro; IPR002819; HD.
DR   InterPro; IPR003607; ME_Pplase_HDc.
DR   InterPro; IPR004811; SpoT_relA.
DR   InterPro; IPR004095; TGS_dom.
DR   Pfam; PF01842; ACT; 1.
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DR   Pfam; PF01966; HD; 1.
DR   Pfam; PF02824; TGS; 1.
DR   SMART; SM00471; HDc; 1.
DR   TIGRFAMs; TIGR00691; spoT_relA; 1.
KW   Transferase; Kinase.
SQ   SEQUENCE   841 AA;  93671 MW;  632A037BA4EF4C94 CRC64;

  Query Match             57.8%;  Score 52;  DB 1;  Length 841;
  Best Local Similarity   60.0%;  Pred. No. 26;
  Matches    9;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           | :| ||  |||'||
Db      50 RPKPAPPERPRPPPP 64


RESULT 14
PTNE_HUMAN
ID   PTNE_HUMAN     STANDARD;      PRT;  1187 AA.
AC   Q15678;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE   (Protein-tyrosine phosphatase pez).
GN   PTPN14 OR PEZ.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast carcinoma;
RX   MEDLINE=95251727; PubMed=7733990;
RA   Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RA   Crompton M.R.;
RT   "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT   ezrin-like domains.";
RL   Biochem. Biophys. Res. Commun. 209:959-965(1995).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF HUMAN TISSUES
CC       INCLUDING KIDNEY, SKELETAL MUSCLE, LUNG AND PLACENTA.
CC   -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X82676; CAA57993.1; -.
DR   HSSP; P29350; 1GWZ.
DR   Genew; HGNC:9647; PTPN14.
DR   MIM; 603155; -.
DR   InterPro; IPR000299; Band_4.1.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   Pfam; PF00373; Band_41; 1.
DR   PRINTS; PR00935; BAND41.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00295; B41; 1.
DR   SMART; SM00194; PTPc; 1.
DR   PROSITE; PS00660; BAND_41_1; 1.
DR   PROSITE; PS00661; BAND_41_2; 1.
DR   PROSITE; PS50057; BAND_41_3; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW   Structural protein; Cytoskeleton; Hydrolase.
FT   DOMAIN       75    239       BAND 4.1-LIKE.
FT   DOMAIN      933   1187       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE   1121   1121       BY SIMILARITY.
FT   DOMAIN      566    573       POLY-PRO.
FT   DOMAIN      709    716       POLY-GLU.
SQ   SEQUENCE   1187 AA;  135239 MW;  015760B75E3574E3 CRC64;

  Query Match             57.2%;  Score 51.5;  DB 1;  Length 1187;
  Best Local Similarity   83.3%;  Pred. No. 42;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       3 RPRPPYLPRPRP 14
           || ||| |||||
Db     565 RPPPPY-PRPRP 575


RESULT 15
PTNE_MOUSE
ID   PTNE_MOUSE     STANDARD;      PRT;  1189 AA.
AC   Q62130;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE   (Protein-tyrosine phosphatase PTP36).
GN   PTPN14.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CB-17-SCID; TISSUE=Thymus;
RX   MEDLINE=94354845; PubMed=8074693;
RA   Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT   "cDNA cloning of a novel protein tyrosine phosphatase with homology
RT   to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
RL   Biochem. Biophys. Res. Commun. 203:479-484(1994).
CC   -!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- TISSUE SPECIFICITY: THYMUS; IN CELLS OF BOTH HEMATOPOIETIC AND
CC       NON-HEMATOPOIETIC ORIGINS.
CC   -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC       TYROSINE PHOSPHATASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D31842; BAA06628.1; -.
DR   HSSP; Q06124; 2SHP.
DR   MGD; MGI:102467; Ptpn14.
DR   InterPro; IPR000299; Band_4.1.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00102; Y_phosphatase; 1.
DR   Pfam; PF00373; Band_41; 1.
DR   PRINTS; PR00935; BAND41.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00295; B41; 1.
DR   SMART; SM00194; PTPc; 1.
DR   PROSITE; PS00660; BAND_41_1; 1.
DR   PROSITE; PS00661; BAND_41_2; 1.
DR   PROSITE; PS50057; BAND_41_3; 1.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
```

```
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
KW   Structural protein; Cytoskeleton; Hydrolase.
FT   DOMAIN       75    239       BAND 4.1-LIKE.
FT   DOMAIN      935   1189       PROTEIN-TYROSINE PHOSPHATASE.
FT   ACT_SITE   1123   1123       BY SIMILARITY.
FT   DOMAIN      566    573       POLY-PRO.
FT   DOMAIN      635    639       POLY-GLY.
FT   DOMAIN      712    718       POLY-GLU.
SQ   SEQUENCE   1189 AA;  135030 MW;  2B85BE5F9C723303 CRC64;

  Query Match             57.2%;  Score 51.5;  DB 1;  Length 1189;
  Best Local Similarity   83.3%;  Pred. No. 42;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       3 RPRPPYLPRPRP 14
           || ||| |||||
Db     565 RPPPPY-PRPRP 575


Search completed: May 13, 2003, 10:40:51
Job time : 13 secs
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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: May 13, 2003, 10:37:02 ; Search time 29 Seconds
(without alignments)
106.576 Million cell updates/sec

Title: US-09-426-011D-3
Perfect score: 90
Sequence: 1 RRRPRPPYLPRPRPP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	67.8	336	12	Q68405	Q68405 human cytom
2	58	64.4	156	10	Q8RV32	Q8rv32 oryza sativ
3	58	64.4	164	6	P79361	P79361 ovis aries
4	58	64.4	190	6	Q9XSQ9	Q9xsq9 capra hircu
5	58	64.4	224	6	O19031	O19031 ovis aries
6	57.5	63.9	183	10	Q94J98	Q94j98 oryza sativ
7	57	63.3	200	16	Q9RK54	Q9rk54 streptomyce
8	57	63.3	361	2	Q9XCG4	Q9xcg4 mycobacteri
9	56	62.2	212	2	O08306	O08306 nocardioide
10	55	61.1	212	12	O41980	O41980 murid herpe
11	55	61.1	464	12	Q91TM2	Q91tm2 tupaia herp
12	54.5	60.6	301	10	Q41848	Q41848 zea mays (m
13	54.5	60.6	2635	12	P88955	P88955 kaposi's sa
14	54.5	60.6	2635	12	O40942	O40942 kaposi's sa
15	54	60.0	347	11	Q8R353	Q8r353 mus musculu
16	54	60.0	359	5	Q9XZT0	Q9xzt0 drosophila
17	54	60.0	427	5	O44582	O44582 caenorhabdi
18	54	60.0	451	5	Q95X63	Q95x63 caenorhabdi
19	54	60.0	955	4	Q9Y2W1	Q9y2w1 homo sapien
20	53.5	59.4	225	11	Q99JA6	Q99ja6 mus musculu
21	53	58.9	168	10	Q9SM77	Q9sm77 oryza sativ
22	53	58.9	184	5	Q23291	Q23291 caenorhabdi
23	53	58.9	185	10	Q94JF6	Q94jf6 oryza sativ
24	53	58.9	199	5	Q8WSY8	Q8wsy8 apis mellif
25	53	58.9	333	10	Q9XIZ3	Q9xiz3 oryza sativ
26	53	58.9	428	10	O23370	O23370 arabidopsis
27	53	58.9	491	10	O82066	O82066 solanum tub
28	53	58.9	520	10	Q9LV14	Q9lv14 arabidopsis
29	52.5	58.3	602	12	Q66852	Q66852 fowl adenov
30	52	57.8	148	16	Q8U5T2	Q8u5t2 agrobacteri
31	52	57.8	155	4	Q96E55	Q96e55 homo sapien
32	52	57.8	439	10	Q42421	Q42421 beta vulgar
33	52	57.8	450	10	Q94CE1	Q94ce1 arabidopsis
34	52	57.8	467	10	Q39184	Q39184 arabidopsis
35	52	57.8	790	5	Q8T458	Q8t458 drosophila
36	52	57.8	1006	10	Q9LMQ1	Q9lmq1 arabidopsis
37	52	57.8	1091	5	Q9W1Z6	Q9w1z6 drosophila
38	51.5	57.2	145	12	Q8V718	Q8v718 simian herp
39	51.5	57.2	238	10	Q8W097	Q8w097 oryza sativ
40	51	56.7	94	5	Q9I7F1	Q9i7f1 drosophila
41	51	56.7	145	10	Q8SAY8	Q8say8 oryza sativ
42	51	56.7	255	10	Q8RYX5	Q8ryx5 oryza sativ
43	51	56.7	409	5	Q9U0Z7	Q9u0z7 leishmania
44	51	56.7	417	5	Q9V4V1	Q9v4v1 drosophila
45	51	56.7	470	10	Q8S5U3	Q8s5u3 oryza sativ

ALIGNMENTS

RESULT 1
Q68405
ID Q68405 PRELIMINARY; PRT; 336 AA.
AC Q68405;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Orf UL151.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOLEDO;
RX MEDLINE=96099416; PubMed=8523595;
RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
RT found in laboratory strains.";
RL J. Virol. 70:78-83(1996).
DR EMBL; U33331; AAA85892.1; -.
SQ SEQUENCE 336 AA; 35116 MW; 9F865E5019F69D0C CRC64;

Query Match 67.8%; Score 61; DB 12; Length 336;
Best Local Similarity 78.6%; Pred. No. 0.94;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy       2 RRPRPPYLPRPRPP 15
           ||| || | |||||
Db     279 RRPIPPILQRPRPP 292
```

RESULT 2
Q8RV32
ID Q8RV32 PRELIMINARY; PRT; 156 AA.
AC Q8RV32;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

```
DE   OSJNBb0032K15.1 protein (OJ1159_D09.32 protein).
GN   OSJNBB0032K15.1 OR OJ1159_D09.32.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
RT   clone:OSJNBb0032K15.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
RT   clone:OJ1159_D09.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003710; BAB86560.1; -.
DR   EMBL; AP003792; BAB89214.1; -.
SQ   SEQUENCE   156 AA;  17659 MW;  4152112C3DB493CF CRC64;

  Query Match             64.4%;  Score 58;  DB 10;  Length 156;
  Best Local Similarity   73.3%;  Pred. No. 1.2;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRPP 15
          |||||||   | |||
Db     78 RRRPRPPLRRRRRPP 92


RESULT 3
P79361
ID   P79361      PRELIMINARY;      PRT;   164 AA.
AC   P79361;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   7.5 kDa bactinecin (Fragment).
GN   BAC7.5.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE=96140581; PubMed=8549789;
RA   Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.;
RT   "Molecular analysis of the sheep cathelin family reveals a novel
RT   antimicrobial peptide.";
RL   FEBS Lett. 377:519-522(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RA   Huttner K.M., Mahoney M.M.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U60598; AAB49713.1; -.
DR   InterPro; IPR001894; Cathelicidin.
DR   Pfam; PF00666; Cathelicidins; 1.
DR   ProDom; PD001838; Cathelicidin; 1.
DR   PROSITE; PS00946; CATHELICIDINS_1; 1.
DR   PROSITE; PS00947; CATHELICIDINS_2; 1.
FT   NON_TER     164    164
SQ   SEQUENCE   164 AA;  18642 MW;  E3BFC871F6AE8B9A CRC64;

  Query Match             64.4%;  Score 58;  DB 6;  Length 164;
  Best Local Similarity   78.6%;  Pred. No. 1.2;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRP 14
          | ||| | ||||||
Db    132 RLRPRRRPRLPRPRP 145


RESULT 4
Q9XSQ9
ID   Q9XSQ9      PRELIMINARY;      PRT;   190 AA.
AC   Q9XSQ9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   Bac7.5 protein.
GN   BAC7.5.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RA   Zhao C., Nguyen T., Brogden K., Lehrer R.;
RT   "cDNA cloning of goat cathelin related peptides.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ243125; CAB45523.1; -.
DR   InterPro; IPR001894; Cathelicidin.
DR   Pfam; PF00666; Cathelicidins; 1.
DR   ProDom; PD001838; Cathelicidin; 1.
DR   PROSITE; PS00946; CATHELICIDINS_1; 1.
DR   PROSITE; PS00947; CATHELICIDINS_2; 1.
FT   CHAIN       131    190       BAC7.5 PROTEIN.
SQ   SEQUENCE   190 AA;  21835 MW;  D13305EF16875F4F CRC64;

  Query Match             64.4%;  Score 58;  DB 6;  Length 190;
  Best Local Similarity   78.6%;  Pred. No. 1.4;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRP 14
          | ||| | ||||||
Db    132 RLRPRRRPRLPRPRP 145


RESULT 5
O19031
ID   O19031      PRELIMINARY;      PRT;   224 AA.
AC   O19031;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   BACTINECIN 11 precursor.
GN   BAC11.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98121317; PubMed=9461419;
RA   Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT   "Localization and genomic organization of sheep antimicrobial peptides
RT   genes.";
RL   Gene 206:85-91(1998).
CC   -!- FUNCTION: ANTIMICROBIAL PEPTIDE (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
DR   EMBL; U77049; AAB62000.1; -.
DR   EMBL; U77046; AAB62000.1; JOINED.
DR   EMBL; U77047; AAB62000.1; JOINED.
DR   EMBL; U77048; AAB62000.1; JOINED.
DR   InterPro; IPR001894; Cathelicidin.
DR   Pfam; PF00666; Cathelicidins; 1.
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DR   ProDom; PD001838; Cathelicidin; 1.
DR   PROSITE; PS00946; CATHELICIDINS_1; 1.
DR   PROSITE; PS00947; CATHELICIDINS_2; 1.
KW   Signal; Antibiotic.
FT   SIGNAL        1     29       POTENTIAL.
FT   PROPEP       30    130       POTENTIAL.
FT   CHAIN       131    224       BACTINECIN 11.
FT   MOD_RES      30     30       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   DISULFID     85     96       BY SIMILARITY.
FT   DISULFID    107    124       BY SIMILARITY.
SQ   SEQUENCE   224 AA;  25669 MW;  6AEAAB1256AC76FC CRC64;

  Query Match             64.4%;  Score 58;  DB 6;  Length 224;
  Best Local Similarity   78.6%;  Pred. No. 1.6;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRP 14
          | ||| | ||||||
Db    132 RLRPRRPRLPRPRP 145


RESULT 6
Q94J98
ID   Q94J98      PRELIMINARY;      PRT;   183 AA.
AC   Q94J98;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   P0047B08.14 protein (OJ1159_D09.5 protein).
GN   P0047B08.14 OR OJ1159_D09.5.
OS   Oryza sativa (Rice), and
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530, 39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT   clone:P0047B08.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
RT   clone:OJ1159_D09.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003053; BAB55690.1; -.
DR   EMBL; AP003792; BAB89188.1; -.
SQ   SEQUENCE   183 AA;  20155 MW;  F1CF823AD89CEB36 CRC64;

  Query Match             63.9%;  Score 57.5;  DB 10;  Length 183;
  Best Local Similarity   73.3%;  Pred. No. 1.6;
  Matches   11;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy      1 RRRPRPPYLPRPRPP 15
          | ||| || |||:||
Db    129 RSRPR-PYAPRPQPP 142


RESULT 7
Q9RK54
ID   Q9RK54      PRELIMINARY;      PRT;   200 AA.
AC   Q9RK54;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein SCO0323.
GN   SCO0323 OR SCF12.02C.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL117669; CAB56128.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   200 AA;  22076 MW;  0DCBBEC5585803B5 CRC64;

  Query Match             63.3%;  Score 57;  DB 16;  Length 200;
  Best Local Similarity   76.9%;  Pred. No. 2;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPR 13
          || | || |||||
Db    118 RRHPEPPALPRPR 130


RESULT 8
Q9XCG4
ID   Q9XCG4      PRELIMINARY;      PRT;   361 AA.
AC   Q9XCG4;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 40.2 kDa protein.
OS   Mycobacterium avium.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1764;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2151;
RA   Eckstein T.M., Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
RT   "Identification of a gene cluster involved in glycopeptidolipid
RT   biosynthesis and of a gene cluster encoding daunorubicin resistance in
RT   two strains of Mycobacterium avium serovar 2.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF143772; AAD44199.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   361 AA;  40208 MW;  AD01DBE825C1C9EA CRC64;

  Query Match             63.3%;  Score 57;  DB 2;  Length 361;
  Best Local Similarity   71.4%;  Pred. No. 3.4;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 RRRPRPPYLPRPRP 14
          |||||||  | | |
Db     32 RRRPRPPAAPHPPP 45


RESULT 9
O08306
ID   O08306      PRELIMINARY;      PRT;   212 AA.
AC   O08306;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 22.7 kDa protein.
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OS   Nocardioides simplex (Arthrobacter simplex).
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Propionibacterineae; Nocardioidaceae; Pimelobacter.
OX   NCBI_TaxID=2045;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IFO12069;
RX   MEDLINE=95319331; PubMed=7596291;
RA   Molnar I., Choi K., Yamashita M., Murooka Y.;
RT   "Molecular cloning, expression in Streptomyces lividans, and analysis
RT   of a gene cluster from Arthrobacter somplex encoding 3-
RT   ketosteroid-.DELTA.1-dehydrogenase, 3-ketosteroid-.DELTA.5-isomerase
RT   and a hypothetical regulatory protein.";
RL   Mol. Microbiol. 15:895-905(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IFO12069;
RA   Dziadek J., Yamashita M., Murooka Y.;
RT   "Cloning, sequencing and characterization of the downstream region of
RT   KsdDI operon of Arthrobacter simplex.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL
CC       REGULATORS.
DR   EMBL; Z93338; CAB07542.1; -.
DR   InterPro; IPR001647; HTH_TetR.
DR   Pfam; PF00440; tetR; 1.
DR   PRINTS; PR00455; HTHTETR.
DR   PROSITE; PS01081; HTH_TETR_FAMILY; 1.
KW   DNA-binding; Hypothetical protein; Transcription regulation.
SQ   SEQUENCE   212 AA;  22740 MW;  F9118E18DDF4E0B2 CRC64;

  Query Match             62.2%;  Score 56;  DB 2;  Length 212;
  Best Local Similarity   73.3%;  Pred. No. 2.8;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           ||||| |   |||||
Db      83 RRRPRGPSGQRPRPP 97


RESULT 10
O41980
ID   O41980      PRELIMINARY;      PRT;   212 AA.
AC   O41980;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Hypothetical 21.9 kDa protein.
GN   GAMMAHV.M13.
OS   murid herpesvirus 4.
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae.
OX   NCBI_TaxID=33708;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WUMS;
RX   MEDLINE=97366649; PubMed=9223479;
RA   Virgin H.W. IV, Latreille P., Wamsley P., Hallsworth K., Weck K.E.,
RA   Dal Canto A.J., Speck S.H.;
RT   "Complete sequence and genomic analysis of murine gammaherpesvirus
RT   68.";
RL   J. Virol. 71:5894-5904(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WUMS;
RA   Latreille P., Wamsley P., Waterston R.H.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U97553; AAB66426.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   212 AA;  21911 MW;  E066860064282149 CRC64;

  Query Match             61.1%;  Score 55;  DB 12;  Length 212;
  Best Local Similarity   75.0%;  Pred. No. 3.8;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 PRPPYLPRPRPP 15
           | || |||| :||
Db     136 PSPPPLPRPQPP 147


RESULT 11
Q91TM2
ID   Q91TM2      PRELIMINARY;      PRT;   464 AA.
AC   Q91TM2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T74.
OS   Tupaia herpesvirus.
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Betaherpesvirinae.
OX   NCBI_TaxID=10397;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2;
RX   MEDLINE=21211637; PubMed=11312357;
RA   Bahr U., Darai G.;
RT   "Analysis and Characterization of the Complete Genome of Tupaia (Tree
RT   Shrew) Herpesvirus.";
RL   J. Virol. 75:4854-4870(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2;
RA   Darai G., Bahr U.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF281817; AAK57119.1; -.
SQ   SEQUENCE   464 AA;  51193 MW;  4BB7313EA2C2BD16 CRC64;

  Query Match             61.1%;  Score 55;  DB 12;  Length 464;
  Best Local Similarity   76.9%;  Pred. No. 7.7;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 RPRPPYLPRPRPP 15
           ||||   ||||||
Db     421 RPRPRPRPRPRPP 433


RESULT 12
Q41848
ID   Q41848      PRELIMINARY;      PRT;   301 AA.
AC   Q41848;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Prolin rich protein.
GN   PRP.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=W64A;
RX   MEDLINE=92361259; PubMed=1498600;
RA   Jose-Estanyol M., Ruiz-Avila L., Puigdomenech P.;
RT   "A maize embryo-specific gene encodes a proline-rich and hydrophobic
RT   protein.";
RL   Plant Cell 4:413-423(1992).
DR   EMBL; X60432; CAA42959.1; -.
DR   HSSP; P24337; 1HYP.
DR   InterPro; IPR003612; AAI.
DR   InterPro; IPR001768; Try/amyl_inhbtr.
DR   Pfam; PF00234; tryp_alpha_amyl; 1.
DR   SMART; SM00499; AAI; 1.
SQ   SEQUENCE   301 AA;  31647 MW;  884EB70854D28C2E CRC64;
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```
  Query Match             60.6%;  Score 54.5;  DB 10;  Length 301;
  Best Local Similarity   71.4%;  Pred. No. 6;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       3 RPRPPYL-PRPRPP 15
           || |||: | ||||
Db     149 RPSPPYVPPTPRPP 162


RESULT 13
P88955
ID   P88955      PRELIMINARY;      PRT;  2635 AA.
AC   P88955;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ORF 64.
OS   Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Rhadinovirus.
OX   NCBI_TaxID=37296;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97094384; PubMed=8939871;
RA   Moore P.S., Boshoff C., Weiss R.A., Chang Y.;
RT   "Molecular mimicry of human cytokine and cytokine response pathway
RT   genes by KSHV.";
RL   Science 274:1739-1744(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97121480; PubMed=8962146;
RA   Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA   Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT   "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT   (HHV8).";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA   Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U75698; AAC57149.1; -.
SQ   SEQUENCE   2635 AA;  289687 MW;  00070132EA8139AF CRC64;

  Query Match             60.6%;  Score 54.5;  DB 12;  Length 2635;
  Best Local Similarity   68.4%;  Pred. No. 44;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    2;

Qy       2 RRPR---PPYLP--RPRPP 15
           ||||   ||| |  |||||
Db     271 RRPRVVIPPYDPTDRPRPP 289


RESULT 14
O40942
ID   O40942      PRELIMINARY;      PRT;  2635 AA.
AC   O40942;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ORF 64.
OS   Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC   Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC   Gammaherpesvirinae; Rhadinovirus.
OX   NCBI_TaxID=37296;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97296220; PubMed=9151804;
RA   Neipel F., Albrecht J.C., Fleckenstein B.;
RT   "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
RT   human herpesvirus 8: determinants of its pathogenicity?";
RL   J. Virol. 71:4187-4192(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA   Friedman-Kien A.E., Fleckenstein B.;
RT   "The genome of human herpesvirus 8 cloned from Kaposi's sarcoma.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U93872; AAB62600.1; -.
SQ   SEQUENCE   2635 AA;  289717 MW;  91DDA0D6FF7B660A CRC64;

  Query Match             60.6%;  Score 54.5;  DB 12;  Length 2635;
  Best Local Similarity   68.4%;  Pred. No. 44;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    2;

Qy       2 RRPR---PPYLP--RPRPP 15
           ||||   ||| |  |||||
Db     271 RRPRVVIPPYDPTDRPRPP 289


RESULT 15
Q8R353
ID   Q8R353      PRELIMINARY;      PRT;  347 AA.
AC   Q8R353;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to thyroid hormone receptor-associated protein, 150 kDa
DE   subunit.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026580; AAH26580.1; -.
KW   Receptor.
SQ   SEQUENCE   347 AA;  38293 MW;  C885A3C2394F4DA6 CRC64;

  Query Match             60.0%;  Score 54;  DB 11;  Length 347;
  Best Local Similarity   60.0%;  Pred. No. 8;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 RRRPRPPYLPRPRPP 15
           || |||  :|:| ||
Db     262 RRSPRPSPVPKPSPP 276


Search completed: May 13, 2003, 10:41:27
Job time : 32 secs
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